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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 17:45:45 ; Search time 15 Seconds
(without alignments)
286.383 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEAQYKAFSAV.....DYDQGRVNYEEFARMIAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726	99.6	146	3 US-08-963-409-1	Sequence 1, Appl1
2	388.5	53.3	149	3 US-08-963-409-3	Sequence 3, Appl1
3	384.5	52.7	149	3 US-08-963-409-4	Sequence 4, Appl1
4	384.5	52.7	149	3 US-08-641-873-20	Sequence 20, Appl1
5	376.5	51.6	642	4 US-08-818-253-2	Sequence 2, Appl1
6	376.5	51.6	642	4 US-08-818-253-2	Sequence 2, Appl1
7	376.5	51.6	652	2 US-08-818-253-4	Sequence 4, Appl1
8	376.5	51.6	652	4 US-08-818-253-4	Sequence 4, Appl1
9	373.5	51.2	642	2 US-08-818-253-6	Sequence 6, Appl1
10	373.5	51.2	642	4 US-08-818-253-6	Sequence 6, Appl1
11	373.5	51.2	656	2 US-08-818-253-8	Sequence 8, Appl1
12	373.5	51.2	656	4 US-08-818-253-8	Sequence 8, Appl1
13	373.5	51.2	152	3 US-08-963-409-5	Sequence 5, Appl1
14	365.5	50.1	142	1 US-07-951-715A-24	Sequence 24, Appl1
15	365.5	50.1	142	2 US-08-459-448A-24	Sequence 24, Appl1
16	365.5	50.1	142	3 US-08-459-595A-24	Sequence 24, Appl1
17	365.5	50.1	142	3 US-08-459-595A-24	Sequence 24, Appl1
18	365.5	50.1	142	3 US-08-459-444-24	Sequence 24, Appl1
19	365.5	50.1	142	4 US-09-547-422-24	Sequence 24, Appl1
20	355.5	48.8	149	1 US-08-100-874-2	Sequence 2, Appl1
21	348.5	47.8	145	4 US-08-720-625-5	Sequence 5, Appl1
22	324.5	44.5	150	4 US-09-239-909-2	Sequence 2, Appl1
23	305.5	41.9	150	4 US-09-239-909-4	Sequence 4, Appl1
24	286.5	39.3	172	4 US-09-285-601-2	Sequence 2, Appl1
25	256	35.1	160	2 US-08-602-941-1	Sequence 1, Appl1
26	256	35.1	160	3 US-08-961-264-1	Sequence 1, Appl1
27	256	35.1	160	4 US-09-442-099A-1	Sequence 1, Appl1

28	254	34.8	163	2	US-08-698-805-8	Sequence 8, Appl1
29	248	34.0	463	1	US-07-951-715A-25	Sequence 25, Appl1
30	248	34.0	463	2	US-08-459-448A-25	Sequence 25, Appl1
31	248	34.0	463	3	US-08-459-595A-25	Sequence 25, Appl1
32	248	34.0	463	3	US-08-459-504B-25	Sequence 25, Appl1
33	248	34.0	463	3	US-08-459-444-25	Sequence 0, Appl1
34	248	34.0	463	4	US-09-547-422-25	Sequence 0, Appl1
35	239.5	32.9	390	3	US-08-993-380-4	Sequence 4, Appl1
36	237.5	32.6	408	1	US-07-951-715A-21	Sequence 21, Appl1
37	237.5	32.6	408	2	US-08-459-448A-21	Sequence 21, Appl1
38	237.5	32.6	408	3	US-08-459-595A-21	Sequence 21, Appl1
39	237.5	32.6	408	3	US-08-459-504B-21	Sequence 21, Appl1
40	237.5	32.6	408	3	US-08-459-444-21	Sequence 21, Appl1
41	237.5	32.6	408	4	US-09-547-422-21	Sequence 21, Appl1
42	237.5	32.6	464	1	US-07-951-715A-22	Sequence 22, Appl1
43	237.5	32.6	464	2	US-08-459-448A-22	Sequence 22, Appl1
44	237.5	32.6	464	3	US-08-459-595A-22	Sequence 22, Appl1
45	237.5	32.6	464	3	US-08-459-504B-22	Sequence 22, Appl1

ALIGNMENTS

RESULT 1
US-08-963-409-1
; Sequence 1, Application US/08963409
; Patent No. 6045315
; GENERAL INFORMATION: Issued 4/4/00
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 317A Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTTUT14
; CLONE: 2743380
; US-08-963-409-1

Query Match 99.6%; Score 726; DB 3; Length 146;
Best Local Similarity 99.3%; Pred. No. 7.4e-69;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

not 100% match
applied art.

QY 1 MAGELTPEEEAQQKAFSAVDTGNGTINAQELGAALKATGKNLSEAQLRKLISEVSDG 60
Db 1 MAGELTPEEEAQQKAFSAVDTGNGTINAQELGAALKATGKNLSEAQLRKLISEVSDG 60
QY 61 DGEISFQFEFLTAARKARAGLEDLQVAFRAFQDGDGHITVDLRRAMAGLQGPLPQOE 120
Db 61 DGEISFQFEFLTAARKARAGLEDLQVAFRAFQDGDGHITVDLRRAMAGLQGPLPQOE 120
QY 121 AMIREADVDDQGRVNYEEFARM 146
Db 121 AMIREADVDDQGRVNYEEFARM 146
RESULT 2
US-08-963-409-3
; Sequence 3, Application US/08963409
; Patent No. 6046315
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 385234
US-08-963-409-3
Query Match 53.3%; Score 388.5; DB 3; Length 149;
Best Local Similarity 52.1%; Pred. No. 1.9e-33;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;
QY 1 MAGELTPEEEAQQKAFSAVDTGNGTINAQELGAALKATGKNLSEAQLRKLISEVSDG 60
Db 1 MADKLTPEEQISEKFAFLFDKDGDTTITTELGTVMRSLGQNPTEAELQDMINEIDTG 60
QY 61 DGEISFQFEFLTAARKAR--AGLEDLQVAFRAFQDGDGHITVDLRRAMAGLQGPLPQOE 117
Db 61 NGTIDFPEFLTMARKLKDRTDEELIEAFRFVDRDGDGYISADELRHVTNLGEKLTNE 120
QY 118 ELDAMIREADVDDQGRVNYEEFARM 143
Db 118 ELDAMIREADVDDQGRVNYEEFARM 143

Db 121 EVDEMIREADIDGQGINYEEFVKMM 146
RESULT 3
US-08-963-409-4
; Sequence 4, Application US/08963409
; Patent No. 6046315
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1334203
US-08-963-409-4
Query Match 52.7%; Score 384.5; DB 3; Length 149;
Best Local Similarity 52.1%; Pred. No. 4.9e-33;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;
QY 1 MAGELTPEEEAQQKAFSAVDTGNGTINAQELGAALKATGKNLSEAQLRKLISEVSDG 60
Db 1 MADQLTPEEQIAEFKFAFLFDKDGDTTITTELGTVMRSLGQNPTEAELQDMINEVDAG 60
QY 61 DGEISFQFEFLTAARKAR--AGLEDLQVAFRAFQDGDGHITVDLRRAMAGLQGPLPQOE 117
Db 61 NGTIDFPEFLTMARKLKDRTDEELIEAFRFVDRDGDGYISADELRHVTNLGEKLTDE 120
QY 118 ELDAMIREADVDDQGRVNYEEFARM 143
Db 121 EVDEMIREADIDGQGINYEEFVKMM 146
RESULT 4
US-08-641-873-20
; Sequence 20, Application US/08641873
; Patent No. 6117976
; GENERAL INFORMATION:
; APPLICANT: Neri, D. GP.


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Db 230 MHDQTEQIAEFKFAFLFDKDGDTTITKELGTVMSLGNPTAEALQDMINEVDADG 289
Qy 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDQDGGHITVDLRRAMAGLQPLPQE 117
Db 290 NGTIYFPEFLTMARKKDTSEIEIRAFRVDKDGNGYISAAELRHVMTNLGEKLTDE 349
Qy 118 ELDAMIRADVDDQGRVNYEEFARM 143
Db 350 EVDEMIREADIDGQGVNYEEFVQM 375

RESULT 7
US-08-818-253-4
; Sequence 4, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-818-253-4

Query Match 51.6%; Score 376.5; DB 2; Length 652;
Best Local Similarity 51.4%; Pred. No. 2.5e-31;
Matches 75; Conservative 32; Mismatches 36; Indels 3; Gaps 2;

Qy 1 MAGELTPEEAQYKFAFSAVTDGNGTINAEQELGALKATGNLSEALRKLISEVSDG 60
Db 230 MHDQTEQIAEFKFAFLFDKDGDTTITKELGTVMSLGNPTAEALQDMINEVDADG 289
Qy 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDQDGGHITVDLRRAMAGLQPLPQE 117
Db 290 NGTIYFPEFLTMARKKDTSEIEIRAFRVDKDGNGYISAAELRHVMTNLGEKLTDE 349
Qy 118 ELDAMIRADVDDQGRVNYEEFARM 143
Db 350 EVDEMIREADIDGQGVNYEEFVQM 375

RESULT 8
US-08-818-252-4
; Sequence 4, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-818-252-4

Query Match 51.6%; Score 376.5; DB 4; Length 652;
Best Local Similarity 51.4%; Pred. No. 2.5e-31;
Matches 75; Conservative 32; Mismatches 36; Indels 3; Gaps 2;

Qy 1 MAGELTPEEAQYKFAFSAVTDGNGTINAEQELGALKATGNLSEALRKLISEVSDG 60
Db 230 MHDQTEQIAEFKFAFLFDKDGDTTITKELGTVMSLGNPTAEALQDMINEVDADG 289
Qy 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDQDGGHITVDLRRAMAGLQPLPQE 117
Db 290 NGTIYFPEFLTMARKKDTSEIEIRAFRVDKDGNGYISAAELRHVMTNLGEKLTDE 349
Qy 118 ELDAMIRADVDDQGRVNYEEFARM 143
Db 350 EVDEMIREADIDGQGVNYEEFVQM 375

RESULT 9
US-08-818-253-6
; Sequence 6, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-818-253-6

Query Match 51.6%; Score 376.5; DB 2; Length 652;
Best Local Similarity 51.4%; Pred. No. 2.5e-31;
Matches 75; Conservative 32; Mismatches 36; Indels 3; Gaps 2;

Qy 1 MAGELTPEEAQYKFAFSAVTDGNGTINAEQELGALKATGNLSEALRKLISEVSDG 60
Db 230 MHDQTEQIAEFKFAFLFDKDGDTTITKELGTVMSLGNPTAEALQDMINEVDADG 289
Qy 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDQDGGHITVDLRRAMAGLQPLPQE 117
Db 290 NGTIYFPEFLTMARKKDTSEIEIRAFRVDKDGNGYISAAELRHVMTNLGEKLTDE 349
Qy 118 ELDAMIRADVDDQGRVNYEEFARM 143
Db 350 EVDEMIREADIDGQGVNYEEFVQM 375
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SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-818-253-6

Query Match 51.2%; Score 373.5; DB 2; Length 642;
Best Local Similarity 50.7%; Pred. No. 5e-31;
Matches 74; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKKAFAVDGNGTINAEALGAALKATGKNLSEAQLRKLISEVDSG 60
DB 230 MHDQLTEEQIAEFKAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 289
QY 61 DGEISFOEFLT-AARKAR--AGLEDLQVAFRAFDGDDGHITVDELRRAAGLGQPLPQE 117
DB 290 NGTIYFPEFLTMARKMKDTSDEEIREAFRVFDKDGNGYISAAQLRHVMTNLGKLTDE 349
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 350 EVDEMIREADIDGQGVNYEEFQVM 375

RESULT 10
US-08-818-252-6
Sequence 6, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 642
TYPE: PRT
ORGANISM: Aequorea victoria
US-08-818-252-6

Query Match 51.2%; Score 373.5; DB 4; Length 642;
Best Local Similarity 50.7%; Pred. No. 5e-31;
Matches 74; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKKAFAVDGNGTINAEALGAALKATGKNLSEAQLRKLISEVDSG 60
DB 230 MHDQLTEEQIAEFKAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 289
QY 61 DGEISFOEFLT-AARKAR--AGLEDLQVAFRAFDGDDGHITVDELRRAAGLGQPLPQE 117
DB 290 NGTIYFPEFLTMARKMKDTSDEEIREAFRVFDKDGNGYISAAQLRHVMTNLGKLTDE 349
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 350 EVDEMIREADIDGQGVNYEEFQVM 375

RESULT 11
US-08-818-253-8
Sequence 8, Application US/08818253
Patent No. 5998204
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 656
TYPE: PRT
ORGANISM: Aequorea victoria
US-08-818-253-8

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-818-253-8

Query Match 51.2%; Score 373.5; DB 2; Length 656;
Best Local Similarity 50.7%; Pred. No. 5.2e-31;
Matches 74; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKKAFAVDGNGTINAEALGAALKATGKNLSEAQLRKLISEVDSG 60
DB 246 MHDQLTEEQIAEFKAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 305
QY 61 DGEISFOEFLT-AARKAR--AGLEDLQVAFRAFDGDDGHITVDELRRAAGLGQPLPQE 117
DB 306 NGTIYFPEFLTMARKMKDTSDEEIREAFRVFDKDGNGYISAAQLRHVMTNLGKLTDE 365
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 366 EVDEMIREADIDGQGVNYEEFQVM 391

RESULT 12
US-08-818-252-8
Sequence 8, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 656
TYPE: PRT
ORGANISM: Aequorea victoria
US-08-818-252-8

Query Match 51.2%; Score 373.5; DB 4; Length 656;
Best Local Similarity 50.7%; Pred. No. 5.2e-31;
Matches 74; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 17:43:00 ; Search time 40 Seconds
(without alignments)
486.365 Million cell updates/sec

Title: us-10-031-403-1

Perfect score: 729

Sequence: 1 MAGETPEEAQYKKAFAV.....DVDQGRVNEEFARMLAQE 146

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_101002.*
- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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 - 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	146	22	AAB67650
2	726	99.6	146	21	Human disease-asso
3	722	99.0	163	22	Novel central nerv
4	722	99.0	163	22	Human polypeptide
5	722	99.0	163	22	Novel human calciu
6	529	72.6	137	21	Breast and ovaria
7	384.5	52.7	149	11	Recombinant calmod
8	384.5	52.7	149	16	Human calmodulin p
9	384.5	52.7	149	21	Human secreted pro
10	384.5	52.7	149	22	Novel human secret

11	384.5	52.7	149	23	AAB57058	Mouse ischaemic co
12	384.5	52.7	149	23	AAU10388	Human calmodulin 1
13	380.5	52.2	149	22	ABB63876	Drosophila melanog
14	380.5	52.2	149	22	ABB66887	Drosophila melanog
15	380.5	52.2	149	22	ABB66889	Drosophila melanog
16	380.5	52.2	375	16	AA78526	GST-calmodulin fus
17	379.5	52.1	148	23	ABB83067	Rat calmodulin ami
18	379.5	52.1	409	16	AA78525	Protein A-calmodul
19	379.5	52.1	535	16	AA78524	Maltose binding pr
20	376.5	51.6	416	23	ABB83069	Calcium sensor G85
21	376.5	51.6	642	19	AA71645	Fluorescent calmod
22	376.5	51.6	652	19	AA71646	Fluorescent calmod
23	373.5	51.2	642	19	AA71647	Fluorescent calmod
24	373.5	51.2	656	19	AA71648	Fluorescent calmod
25	370.5	50.8	151	9	AA80162	Biosynthetic multi
26	365.5	50.1	143	23	ABB83312	Partial calmodulin
27	361.5	49.6	146	21	AA50796	Human calmodulin/N
28	357.5	49.0	149	21	AA50797	Human calmodulin/N
29	355.5	48.8	149	17	AA81571	Potato calmodulin.
30	355.5	48.8	149	21	AA22934	Arabidopsis thalia
31	355.5	48.8	182	21	AA22933	Arabidopsis thalia
32	352.5	48.4	149	21	AA09210	Arabidopsis thalia
33	352.5	48.4	149	21	AA19559	Arabidopsis thalia
34	352.5	48.4	149	21	AA36517	Arabidopsis thalia
35	352.5	48.4	149	21	AA36788	Arabidopsis thalia
36	352.5	48.4	149	21	AA38370	Arabidopsis thalia
37	352.5	48.4	149	21	AA48103	Arabidopsis thalia
38	352.5	48.4	149	21	AA48200	Arabidopsis thalia
39	352.5	48.4	151	21	AA48102	Arabidopsis thalia
40	352.5	48.4	151	21	AA48199	Arabidopsis thalia
41	352.5	48.4	159	21	AA38438	Arabidopsis thalia
42	352.5	48.4	160	21	AA36787	Arabidopsis thalia
43	352.5	48.4	182	21	AA40532	Arabidopsis thalia
44	324.5	44.5	136	21	AA77954	A. thaliana enviro
45	324.5	44.5	150	21	AA95249	Soybean calmodulin

ALIGNMENTS

RESULT 1

AA867650
ID AAB67650 standard; Protein; 146 AA.

AC AAB67650;

XX AAB67650;

DT 29-MAY-2001 (first entry)

XX Amino acid sequence of a human calmodulin-like skin protein.

DE Human; calmodulin-like skin protein; CLSP; epidermal differentiation;
KW calcium-mediated signal pathway; epidermal proliferation; dry skin;
KW hyperkeratosis; parakeratosis; psoriasis; ichthyosis; neoplasia;
KW skin aging; skin damage.

XX Homo sapiens.

OS Homo sapiens.

XX FR2796646-A1.

XX 26-JAN-2001.

PF 23-JUL-1999; 99FR-0009615.

XX 23-JUL-1999; 99FR-0009615.

XX (OREA) L'OREAL SA.

XX Mehul B, Bernard D, Simonetti L;

XX WPI; 2001-184569/19.

XX N-PSDB; AAF55621.

XX New polypeptide isolated from human skin and having calcium fixing

XX 05-JUN-2002 (first entry)
DT Novel central nervous system protein #488.
DE
DE
XX
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
XX
PN WO200155318-A2.
XX
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PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01332.
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XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-581633/65.
DR N-PSDB; ABK43908.
XX
PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives -
XX
PS Claim 9; SEQ ID No 1096; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein, (II) and polypeptides (III) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 99.0%; Score 722; DB 22; Length 163;
Best Local Similarity 98.6%; Pred. No. 1e-66;
Matches 144; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 61 DGEISQFELTAARAGLEQLQVAFRAFDQDGDGHTVDELRRAMAGLQGPLQPEELD 120
Db 78 DGEISQFELTAARAGLEQLQVAFRAFDQDGDGHTVDELRRAMAGLQGPLQPEELD 137
QY 121 AMIREADVQDGRVNYEEFARLAGE 146
Db 138 AMIREADVQDGRVNYEEFARLAGE 163
RESULT 4
ID AAM43627
XX AAM43627 standard; Protein; 163 AA.

AC AAM43627;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 305.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 30-AUG-2000; 2000US-0227009.
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PR 06-SEP-2000; 2000US-0230438.
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PR 08-SEP-2000; 2000US-0231244.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.

KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide.

XX Homo sapiens.

OS WO200155304-A2.

PN 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US01302.

PE 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

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PR 07-JUL-2000; 2000US-0216647.

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PR 11-JUL-2000; 2000US-0217487.

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PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

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PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.

PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.

PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241826.

PR 01-NOV-2000; 2000US-0244617.

PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.

PR 08-NOV-2000; 2000US-0246477.

PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.

PR 08-NOV-2000; 2000US-0246525.

PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.

PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.

PR 08-NOV-2000; 2000US-0246611.

PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.

PR 17-NOV-2000; 2000US-0249209.

PR 17-NOV-2000; 2000US-0249210.

PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.

PR 17-NOV-2000; 2000US-0249213.

PR 17-NOV-2000; 2000US-0249214.

PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.

PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249246.

PR 17-NOV-2000; 2000US-0249254.

PR 17-NOV-2000; 2000US-0249255.

PR 17-NOV-2000; 2000US-0249257.

PR 17-NOV-2000; 2000US-0249297.

PR 01-DEC-2000; 2000US-0250160.

PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.

PR 06-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.

PR 08-DEC-2000; 2000US-0251868.

PR 08-DEC-2000; 2000US-0251869.


```

XX PN JP02092286-A.
XX XX
XX PD 03-APR-1990.
XX XX
XX PF 30-SEP-1988; 88JP-0246239.
XX XX
XX PR 30-SEP-1988; 88JP-0246239.
XX XX
XX PA (KIRI ) KIRIN BREWERY KK.
XX XX
XX DR WPI; 1990-144900/19.
XX DR N-PSDB; AAQ04331.
XX XX
XX PT Calmodulin prepn. - by culturing transformed E. coli.
XX XX
XX PS Disclosure; ; p; Japanese.
XX XX
XX CC The recombinant calmodulin is produced by cloning the gene into an
XX CC expression vector and culturing to produce the protein.
XX CC See also AAQ04332-4.
XX XX
XX SQ Sequence 149 AA;

Query Match 52.78; Score 384.5; DB 11; Length 149;
Best Local Similarity 52.18; Pred. No. 6.7e-32;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

QY 1 MAGELTPEEEAQYKAFSAVDTDCNGTINAQELGAALKATGKNLSEAOQLRLKLISEVSDG 60
DB 1 MADQLTEQIAEFKAEFSLFDKDGDTTITTKELGTVMRSLGQNTPEALQDMINEVDADG 60
QY 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDQDGDGHITVDLRRAMAGLQPLPQE 117
DB 61 NGTIDFPEFLTMARKMKDTSDEEIREAFRVDKNGYISAAELRHVMTNLGEKLTDE 120
QY 118 ELDAWIREADVDDQGRVNYEEFARM 143
DB 121 EVDEMIREADIDGQGVNYEEFVQMM 146

RESULT 9
AAG03832
ID AAG03832 standard; Protein; 149 AA.
XX AC AAG03832;
XX XX
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 7913.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX XX
XX OS Homo sapiens.
XX XX
XX PN EP1033401-A2.
XX XX
XX PD 06-SEP-2000.
XX XX
XX PF 21-FEB-2000; 2000EP-0200610.
XX XX
XX PR 26-FEB-1999; 99US-0122487.
XX XX
XX PA (GEST ) GENSET.
XX XX
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX DR N-PSDB; AAC03838.
XX XX
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX XX
XX PS Claim 13; SEQ ID 7913; 71pp + CD-ROM; English.
XX XX
XX CC The present sequence is a polypeptide encoded by one of a large number

```

CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.

XX Sequence 149 AA;

Query Match 52.7%; Score 384.5; DB 21; Length 149;
 Best Local Similarity 52.1%; Pred. No. 6.7e-32;
 Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDTCNGTINAEIGALGALKATGKNLSEAOQLRLKLISEVSDG 60

Db 1 MADQLTEEQIAEFKAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELODMINEVDADG 60

QY 61 DGEISFOEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDLRRAMAGLGLOPLQE 117

Db 61 NGTIDPEFLTMMARKMKDTSDEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARM 143

Db 121 EVDEMIREADIDGQGVNYEEFQVM 146

RESULT 10

AAU28050

ID AAU28050 standard; Protein; 149 AA.

XX AC AAU28050;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secretory protein, Seq ID No 219.

XX KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW ankyrotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

XX OS Homo sapiens.

XX PN WO200166689-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.

XX PR 19-MAY-2000; 2000US-0574454.

XX PR 17-JUN-2000; 2000US-0596193.

XX PR 14-JUL-2000; 2000US-0616847.

XX PR 19-SEP-2000; 2000US-0665363.

XX PR 20-OCT-2000; 2000US-0693267.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

XX PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX XX WPI; 2001-589934/66.

DR

DR N-PSDB; AAS44950.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 3; SEQ ID No 219; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.

SQ Sequence 149 AA;

Query Match 52.7%; Score 384.5; DB 22; Length 149;

Best Local Similarity 52.1%; Pred. No. 6.7e-32;

Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDTCNGTINAEIGALGALKATGKNLSEAOQLRLKLISEVSDG 60

Db 1 MADQLTEEQIAEFKAFSLFDKDGDTITTKELGTVMRSLGQNPTEAELODMINEVDADG 60

QY 61 DGEISFOEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDLRRAMAGLGLOPLQE 117

Db 61 NGTIDPEFLTMMARKMKDTSDEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARM 143

Db 121 EVDEMIREADIDGQGVNYEEFQVM 146

RESULT 11

ABB57058

ID ABB57058 standard; Protein; 149 AA.

XX AC ABB57058;

XX DT 07-MAR-2002 (first entry)

XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:112.

XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX OS Mus musculus.
XX PN WO200188188-A2.
XX XX
XX PD 22-NOV-2001.
XX XX
XX PF 18-MAY-2001; 2001WO-JP04192.
XX XX
XX PR 18-MAY-2000; 2000JP-0145977.
XX XX
XX PA (DYN1-) UNIV NIHOON SCHOOL JURIDICAL PERSON.
XX PI
XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX DR WPI; 2002-034733/04.
XX DR N-PSDB; ABI99274.
XX XX
XX XX
XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX PT expression levels of particular genes defined in the specification or
XX PT by determining the expression profile of a gene group comprising these
XX PT genes -
XX PS
XX PS Claim 2; Page 322; 2690pp; English.
XX CC The present invention describes a method for examining ischaemic
XX CC conditions, comprising measuring the expression levels of particular
XX CC genes (I) in a test sample or determining the expression profile of a
XX CC gene group in the sample comprising genes selected from (I). The method
XX CC is useful for examining the ischaemic condition (e.g. compressive
XX CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX CC expression levels of particular genes (ABI99202 to ABI9912, encoding
XX CC the protein sequences in ABB57020 to ABB57374) or by determining the
XX CC expression profile of a gene group comprising these genes. The
XX CC expression levels or expression profiles produced by these genes are
XX CC used as an indicator when screening for ischaemic condition-improving
XX CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914
XX CC represent PCR primers for a mouse ischaemic condition related sequence,
XX CC which are used in the exemplification of the present invention.
XX SQ Sequence 149 AA;
Query Match 52.7%; Score 384.5; DB 23; Length 149;
Best Local Similarity 52.1%; Pred. No. 6.7e-32;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;
Qy 1 MAGELTPPEEAQYKFAFSAVTDGNGTINAOELGAALKATGKNLSEALRLKLISEVSDG 60
Db 1 MADQLTEEQIAEFKFAFSLFDKDGDTTITTELGTVMRSLGQNPTEAELODMINEVDAG 60
Qy 61 DGEISFQEFLLT-AARKAR--AGLEDQVAFRAFDQDGDGHITVDLRRAMAGLGQPLQOE 117
Db 61 NGTIDFPEFLTMARKMKDTSDEEIREAFRVFDKNGYISAAELRHVMTNLGKLTDE 120
Qy 118 ELDAMIREADVDDQGRVNYEEFARM 143
Db 121 EVDAMIREADVDDQGRVNYEEFARM 146
RESULT 12
AAU10388
ID AAU10388 standard; Protein; 149 AA.
XX AC AAU10388;
XX XX
XX DT 26-FEB-2002 (first entry)
XX XX
XX DE Human calmodulin 1 (CALM1).
XX XX Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
XX KW haplotyping; SCVA3; Alzheimer's disease; drug screening;
XX KW calcium-dependent signal transduction.

OS Homo sapiens.
XX PN WO200179218-A2.
XX XX
XX PD 25-OCT-2001.
XX XX
XX PF 09-APR-2001; 2001WO-US11509.
XX XX
XX PR 12-APR-2000; 2000US-196340P.
XX XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI
XX PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX DR WPI; 2002-049190/06.
XX DR N-PSDB; AAS17569, AAS17570.
XX XX
XX PT New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
XX PT expressing CALM1 protein for use in screening for candidate drugs to
XX PT treat diseases related to CALM1 activity such as Alzheimer's disease.
XX PS Disclosure; Fig 4; 82pp; English.
XX CC The invention relates to an isolated polynucleotide comprising a
XX CC sequence selected from a polymorphic variant of calmodulin 1 (CALM1).
XX CC The polymorphic variant comprises an CALM1 isogene defined by a
XX CC haplotype selected from haplotypes 1-21 given in the specification.
XX CC The polymorphisms are useful for studying the biological function of
XX CC CALM1 as well as in identifying drugs targeting this protein for the
XX CC treatment of a disorder related to its abnormal expression or function.
XX CC The polymorphic variants may also be used in screening for compounds
XX CC targeting CALM1 to treat a specific condition or disease predicted to
XX CC be associated with CALM1 activity. Establishing CALM1 haplotype or
XX CC haplotype pair of an individual is useful for improving the efficiency
XX CC and reliability of several steps in the discovery and development of
XX CC drugs for treating diseases associated with SCVA3 activity, e.g.
XX CC Alzheimer's disease and diseases involving defects in calcium-dependent
XX CC signal transduction. Haplotyping the CALM1 gene in an individual is
XX CC also useful in the design of clinical trials of candidate drugs for
XX CC treating a specific condition or disease predicted to be associated
XX CC with CALM1 activity. The present sequence represents the amino acid
XX CC sequence of human CALM1.
XX SQ Sequence 149 AA;
Query Match 52.7%; Score 384.5; DB 23; Length 149;
Best Local Similarity 52.1%; Pred. No. 6.7e-32;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;
Qy 1 MAGELTPPEEAQYKFAFSAVTDGNGTINAOELGAALKATGKNLSEALRLKLISEVSDG 60
Db 1 MADQLTEEQIAEFKFAFSLFDKDGDTTITTELGTVMRSLGQNPTEAELODMINEVDAG 60
Qy 61 DGEISFQEFLLT-AARKAR--AGLEDQVAFRAFDQDGDGHITVDLRRAMAGLGQPLQOE 117
Db 61 NGTIDFPEFLTMARKMKDTSDEEIREAFRVFDKNGYISAAELRHVMTNLGKLTDE 120
Qy 118 ELDAMIREADVDDQGRVNYEEFARM 143
Db 121 EVDAMIREADVDDQGRVNYEEFARM 146
RESULT 13
ABB63876
ID ABB63876 standard; Protein; 149 AA.
XX AC ABB63876;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX Drosophila melanogaster polypeptide SEQ ID NO 18420.
XX XX Drosophila; developmental biology; cell signalling; insecticide;

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY .
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL10992.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 27459; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 149 AA;

Query Match 52.2%; Score 380.5; DB 22; Length 149;
Best Local Similarity 51.0%; Pred. No. 1.7e-31;
Matches 76; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDGTGNGTINAQELGAALKATGKLNLSAQLRKLISEVDSG 60
DB 1 MADQLTEQIAEFKEAFLPKDGGDTTITKELGTVNRSLGQNFTAEQLQMINVEDADG 60

QY 61 DGEISFOEFLT-AAARKAR--AGLEDLQVAFRAFDQDGDGHITVDLRRAMAGLQPLPQE 117
DB 61 NGTIDFPEFLTMAKMKDSTDSEEEIREAFRVFDKNGGFTISAAELRHVMTNLGKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARMLAQE 146
DB 121 EVDEMIREADIDGDGVNYEEFVTMTSK 149

Search completed: March 24, 2003, 17:44:07
Job time : 41 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run On: March 24, 2003, 17:44:35 ; Search time 19 Seconds
(without alignments)
738.717 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729

Sequence: 1 MAGELTPPEAQYKKAFAV.....DYDQGRVNYEEFARMALQAE 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: -pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	388.5	53.3	148	1 MCXAM	calmodulin - sea a
2	388.5	53.3	149	1 MCZOF	calmodulin - malar
3	385.5	52.9	148	1 MCSW	calmodulin - scall
4	384.5	52.7	149	1 MCHU	calmodulin [valida
5	384.5	52.7	149	1 MCRT	calmodulin [valida
6	384.5	52.7	149	1 MCCH	calmodulin - chick
7	384.5	52.7	149	1 I51202	calmodulin - duck
8	384.5	52.7	149	2 JCI305	calmodulin - Japan
9	384.5	52.7	149	2 I51402	calmodulin - Afric
10	384.5	52.7	149	2 S37707	calmodulin - mouse
11	383.5	52.6	147	1 MCZJR	calmodulin - sea p
12	382.5	52.5	149	1 MCEE	calmodulin - elect
13	380.5	52.2	148	1 MCAZS	calmodulin - sea s
14	380.5	52.2	149	1 MCFE	calmodulin [valida
15	380.5	52.2	149	1 MCGAC	calmodulin - Calif
16	379.5	52.1	148	1 MCBQ	calmodulin [valida
17	379.5	52.1	148	1 MCON	calmodulin - salmo
18	379.5	52.1	149	2 T31737	hypothetical prote
19	378.5	51.9	148	1 MCSFCU	calmodulin - sea c
20	378.5	51.9	149	2 I49567	calmodulin - mouse
21	375.5	51.5	148	1 MCLQ	calmodulin - migra
22	374.5	51.4	148	1 MCRB	calmodulin - rabbi
23	373.5	51.2	149	2 S53019	calmodulin - Macro
24	371.5	51.0	141	2 S02690	calmodulin A - sea
25	371.5	51.0	149	1 MCTUC	calmodulin - Trypa
26	370.5	50.8	149	1 MCTE	calmodulin - Tetra
27	370.5	50.8	149	1 MCUTG	calmodulin - Trypa
28	370.5	50.8	149	2 JCI309	calmodulin - Stylo
29	370.5	50.8	149	2 A48111	calmodulin C - Try

30	370.5	50.8	149	2 S28954	calmodulin - Tetra
31	369.5	50.7	163	1 MCRM	calmodulin - Chlam
32	367.5	50.4	148	1 MCMRP	calmodulin - cornu
33	367.5	50.4	149	1 MCPP	calmodulin - Param
34	365.5	50.1	149	1 MCMAX	calmodulin - Achly
35	365.5	50.1	151	1 MCDO	calmodulin - slime
36	364.5	50.0	148	1 MCEG	calmodulin - Eugle
37	363.5	49.9	149	1 MCCRM	calmodulin, striat
38	358.5	49.2	148	2 JCI1094	calmodulin - rice
39	358.5	49.2	149	1 MCBH	calmodulin - barle
40	358.5	49.2	149	1 MCAA	calmodulin - alfal
41	358.5	49.2	149	2 S24952	calmodulin 1 (clon
42	358.5	49.2	149	2 S51933	calmodulin cam2 -
43	357.5	49.0	148	1 MCSP	calmodulin - spina
44	357.5	49.0	149	1 MCHNB	calmodulin-related
45	355.5	48.8	138	2 S02691	calmodulin B - sea

ALIGNMENTS

RESULT 1

MCXAM

calmodulin - sea anemone (Metridium senille) (tentative sequence)

N;Alternate names: modulator protein

C;Species: Metridium senille (brown sea anemone, filled sea anemone)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Nov-1999

C;Accession: A90223; A03023

R;Takagi, T.; Nemoto, T.; Konishi, K.; Yazawa, M.; Yagi, K.

Biochem. Biophys. Res. Commun. 96, 377-381, 1980

A;Title: The amino acid sequence of the calmodulin obtained from sea anemone (Metridi

A;Reference number: A90223; MUID:81062446; PMID:6108109

A;Accession: A90223

A;Molecule type: protein

A;Residues: 1-148 <AK>

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; methylated amin

F;7-39/Domain: calmodulin repeat homology <EF1>

F;43-75/Domain: calmodulin repeat homology <EF2>

F;80-112/Domain: calmodulin repeat homology <EF3>

F;116-148/Domain: calmodulin repeat homology <EF4>

F;1/Modified site: blocked amino end (Ala) #status experimental

F;20,22,24,26,31/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted

F;56,58,60,62,67/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted

F;93,95,97,99,104/Binding site: calcium (Asp, Asp, Phe, Glu) #status predicted

F;115/Modified site: N6,N6-trimethyllysine (Lys) #status experimental

F;129,131,133,135,140/Binding site: calcium (Asp, Asp, Gln, Glu) #status predict

Query Match 53.3%; Score 388.5; DB 1; Length 148;

Best Local Similarity 52.0%; Pred. No. 1.4e-20;

Matches 77; Conservative 30; Mismatches 38; Indels 3; Gaps 2;

QY 2 AGELTPPEAQYKKAFAVDTDGNTINAOELGAALAKATGNLSEAOQLKILISVDSGDG 61

Db 1 ADQTEQIAEFKFAFLFKDGDGTTTRELGVVMSLGNPTPEAEIQDINEVDADGD 60

QY 62 GEISFOEFLT-AARKAR--AGLEDQVAFRAFDGDGHITVDRLRAMAGLGPQLPQEE 118

Db 61 GTIDFPPELTMARKMKDTSDEEIREAFRVFDKDGDFISAAELRHVMTNLGEKLTDDE 120

QY 119 LDAMIRADVDDQGRVNYEEFARMALQAE 146

Db 121 VDEMIREADIDGQGVNYEEFVKMTSK 148

RESULT 2

MCZOF

calmodulin - malaria parasite (Plasmodium falciparum)

N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina

C;Species: Plasmodium falciparum

C;Date: 22-Apr-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C;Accession: B45994; A49774; S21813

R;Robson, K.J.; Jennings, M.W.

F;1/Modified site: acetylated amino end (Ala) #status experimental
F;20,22,26,31/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted
F;56,58,60,62,67/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted
F;93,95,97,99,104/Binding site: calcium (Asp, Asp, Phe, Glu) #status predicted
F;115/Modified site: N6,N6-trimethyllysine (Lys) #status experimental
F;129,131,133,135,140/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

Query Match 52.9%; Score 385.5; DB 1; Length 148;
Best Local Similarity 52.0%; Pred. No. 2.3e-20;
Matches 77; Conservative 29; Mismatches 39; Indels 3; Gaps 2;

QY 2 AGELTPEEEAOYKAFSAVDTDGNGTINAQELGAALKATGNLSERASQLRLKIIEVSDGD 61
 | :| |:||:|||:| |||:||||| :|| :|| :|| :|| :|| :|| :|| :||
Db 1 ADOLTEQTAEFEARSLFDKDGDTITTKELGVRSUGQNPTAEALQMINEVDADGD 60

QY 62 GETISOEFFLT-AARKA--AGLEDLVAFRAFDQDGHITVDLERRANAGLOPLPOEE 118
 | :| |:|||:| ||| :||||| :|| :|| :|| :|| :|| :|| :|| :||
Db 61 GTIDDFEFLTMARKMKDTSDEEIRAEFRVKDKDGFISAAELRHVVNTLGKLTDEE 120

QY 119 LDMIREADVDDGRVNYEFARMIAQE 146
 | :| |:|||:| |||:||||| | : :
Db 121 VDEMIREADDIDGGQVNYEEFTVMITSK 148

RESULT 4
MCHU
calmodulin [validated] - human
N:Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kinase
C:Species: Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 30-Jun-1992 #text_change 15-Sep-2000
C:C-accession: S48728; S13159; A31787; J28479; A90460; JN0365; I52348; A03021
R:Rhynier, J.A.; Ottiger, M.; Wicki, R.; Greenwood, T.M.; Strehler, E.E.
Eur. J. Biochem. 225, 71-82, 1994
A>Title: Structure of the human CALML calmodulin gene and identification of two CALMI
A:Structure number: S48728; UID:95010144; PMID:7925473
A:Accession: S48728
A:Molecule type: DNA
A:Residues: 1-149 <RHY>
A:A-Cross-references: EMBL:U11886; NID:g531824; EMBL:UI1022; NID:g531825; PIDN:AAA60644
A:Genetics: CAL1
R:Koller, M.; Schnyder, B.; Strehler, E.E.
Biochim. Biophys. Acta 1087, 180-189, 1990
A>Title: Structural organization of the human CAMIII calmodulin gene.
A:Reference number: S13159; UID:91027929; PMID:2223680
A:Accession: S13159
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:A-Cross-references: EMBL:X52606; EMBL:X52607; EMBL:X52608; NID:g29637; PIDN:CAA36839.
A:Genetics: CAL3
R:Fischer, R.; Koller, M.; Flura, M.; Mathews, S.; Strehler-Page, M.A.; Krebs, J.; Pe
J. Biol. Chem. 263, 17055-17062, 1988
A>Title: Multiple divergent mRNAs code for a single human calmodulin.
A:Reference number: A31787; UID:89034207; PMID:3182832
A:Accession: A31787
A:Molecule type: mRNA
A:Residues: 1-149 <FS>
A:A-Cross-references: GB:J04046; NID:g179887; PIDN:AAA51918.1; PID:g179888
A:Genetics: CAL1
R:Sengupta, B.; Friedberg, F.; Detera-Wadleigh, S.D.
J. Biol. Chem. 262, 16663-16670, 1987
A>Title: Molecular analysis of human and rat calmodulin complementary DNA clones. Evi
A:Reference number: A92620; UID:88059053; PMID:2445749
A:Accession: A28479
A:Molecule type: mRNA
A:Residues: 1-149 <SEN>
A:A-Cross-references: GB:J03468; GB:M19311; NID:g179883; PIDN:AAA35641.1; PID:g179884
A:Genetics: CAL2
R:Sasagawa, T.; Ericsson, L.H.; Walsh, K.A.; Schreiber, W.E.; Fischer, E.H.; Titani,
Biochemistry 21, 2565-2569, 1982
A>Title: Complete amino acid sequence of human brain calmodulin.
A:Reference number: A90460; UID:82231946; PMID:7093203
A:Accession: A90460
A:Molecule type: protein

QY 1 MAGELTPEEEAQYKAFSAVDTGNGTTINAEGLCAALKATGNLSAQLRKLISEYSDSG 60
|| || || || || || || || || || || || || || || || || || || || || || ||
Db 1 MADOLTEEQIAEFKEAFSLFDKGDDGTITTKELGTVMRSLGQNPTAEALQDMINEVDADG 60

QY 61 DGRISQFEFLT-AARKAR--AGLEDLOVAFRATDQGDGHITVDLRRAMAGLGQPLOQE 17
:|| || || || || || || || || || || || || || || || || || || || || || ||
Db 61 NGTDIPFETLMARKMKDTSDEEAREAFVRFDKNGYISAELRHVTNLTGEKLDTDE 120

QY 118 ELDMIREADVDDODGRVNVEEFARM 143
|:| ||||||| |:| ||||||| |:|
Db 121 EVDEMIREADDIDGGQNVVEEFQM 146

RESULT 5
MCRT
calmodulin [validated] - rat
N;Alternate names: modulator protein; phosphodiesterase activator; phospho
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Sep-200
C;Accession: S03206; A30899; S05228; I57616; B28479; A29082; S1753
R;Nojima, H.; Sokabe, H.
J. Mol. Biol. 193, 439-445, 1987
A;Title: Structure of a gene for rat calmodulin.
A;Reference number: S03206; MUID:87226204; PMID:3035194
A;Accession: S03206
A;Molecule type: DNA
A;Residues: 1-149 <NOI>
A;Cross-references: EMBL:X13931; NID:g55860; PIDN:CAA32119.1; PID:g1334203
A;Experimental source: strain Wistar-Kyoto
A;Genetics: CAM1
A;Accession: A30899
A;Molecule type: mRNA
A;Residues: 1-149 <NO>
A;Cross-references: EMBL:X13933; NID:g57040; PIDN:CAA32120.1; PID:g57041
A;Experimental source: strain Sprague-Dawley
R;Nojima, H.
J. Mol. Biol. 208, 269-282, 1989
A;Title: Structural organization of multiple rat calmodulin genes.
A;Reference number: S05227; MUID:89362474; PMID:2527998
A;Accession: S05228
A;Molecule type: DNA
A;Residues: 1-149 <NO>
A;Cross-references: EMBL:X14265; NID:g55866; PIDN:CAA32478.1; PID:g55867
A;Genetics: CAM2
A;Accession: S05227
A;Molecule type: DNA
A;Residues: 1-149 <NO>
A;Cross-references: EMBL:X13833; NID:g55863; PIDN:CAA32062.1; PID:g818020
A;Genetics: CAM3
R;Nojima, H.; Kishi, K.; Sokabe, H.
Mol. Cell. Biol. 7, 1873-1880, 1987
A;Title: Multiple calmodulin mRNA species are derived from two distinct ge
A;Reference number: I57616; MUID:87257889; PMID:3037336
A;Accession: I57616
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <NO3>
A;Cross-references: GB:M17069; NID:g203257; PIDN:AAA40863.1; PID:g203258
R;Sengupta, B.; Friedberg, F.; Detex-Wadleigh, S.D.
J. Biol. Chem. 262, 16663-16670, 1987
A;Title: Molecular analysis of human and rat calmodulin complementary DNA
A;Reference number: A95620; MUID:88059053; PMID:2445749
A;Accession: B28479
A;Molecule type: mRNA
A;Residues: 1-149 <SEN>
R;Sherbany, A.A.; Parent, A.S.; Brosius, J.
DNA 6, 267-272, 1987
A;Title: Rat calmodulin cDNA.
A;Reference number: A29082; MUID:87246077; PMID:2885164
A;Accession: A29082
A;Molecule type: mRNA

Query Match
Best Local S
Matches 76

[illegible]

Db 122 EMIREADIDGQGVNYEEFYKMMTSK 147

RESULT 12

MCEE

calmodulin - electric eel

N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kinase; Electrophorus electricus (electric eel)

C;Date: 25-Feb-1985 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999

C;Accession: A03022; A60781; I50534

R;Lagace, L.; Chandra, T.; Woo, S.L.C.; Means, A.R.

J. Biol. Chem. 258, 1684-1688, 1983

A;Title: Identification of multiple species of calmodulin messenger RNA using a full

A;Reference number: A03022; MUID:83108962; PMID:6185488

A;Accession: A03022

A;Molecule type: mRNA

A;Residues: 1-149 <LAG>

A;Cross-references: GB:J009331; NID:g213131

A;Experimental source: electroplax

A;Note: This ORF is not annotated in GenBank entry ELCCALMA, release 103

R;Toda, H.; Abe, Y.; Yazawa, M.; Yagi, K.

Seikagaku 57, 1037, 1985

A;Title: Amino acid sequence of sea cucumber calmodulin.

A;Reference number: JK0011

A;Note: author-supplied citation

A;Accession: A60781

A;Molecule type: protein

A;Residues: 2-74, 'R' 76-149 <YAZ>

A;Note: 75-Lys also found

R;Iida, Y.

Bull. Chem. Soc. Jpn. 57, 2667-2668, 1984

A;Title: cDNA sequences and molecular evolution of calmodulin genes of chicken and eel

A;Reference number: I50184

A;Accession: I50534

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-149 <IID>

A;Cross-references: GB:M36168; NID:g213129; PIDN:AAA49236.1; PID:g213130

C;Comment: This protein has multiple, calcium-dependent, regulatory activities in var

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: calcium binding; duplication; EF hand; methylated amino acid

F;2-149/Product: calmodulin #status predicted <MAT>

F;8-40/Domain: calmodulin repeat homology <EF1>

F;44-76/Domain: calmodulin repeat homology <EF2>

F;81-113/Domain: calmodulin repeat homology <EF3>

F;117-149/Domain: calmodulin repeat homology <EF4>

F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted

F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Thr, Glu) #status predicted

F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Tyr, Glu) #status predicted

F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

Query Match 52.5%; Score 382.5; DB 1; Length 149;

Best Local Similarity 50.7%; Pred. No. 3.8e-20;

Matches 74; Conservative 31; Mismatches 38; Indels 3; Gaps 1;

Qy 1 MAGELTPEERAAQYKKPASYDTGNGCTINAEQLGAALKATGKNLSEAQLRLISEYVDSG 60

Db 1 MADQLTEQAEKFAEFLSKDGDGDTTITKELTGVTSLGQNPTEAELODMINEVDAG 60

Qy 61 DGEISFQEFLETAARKAGEL---EDLQVAPRAFQDQGDGHITVDELRRAAGLGGQLPOE 117

Db 61 NGTIDFPEFLTMAKMKNDTDEEIREAFRVFDKDGNGYISAEELRHVNTNIGEKLTDE 120

Qy 118 ELDMIREADVDDQGRVNYEEFARM 143

Db 121 EVDEMIREADIDGQGVNYEEFYQMM 146

RESULT 13

MCAZS

calmodulin - sea squirt

N;Alternate names: modulator protein

F:116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F:130,132,134,136,141/Binding site: calcium (Asp, Asp, Gln, Glu) #status predicted

Query Match 52.2%; Score 380.5; DB 1; Length 149;
Best Local Similarity 51.0%; Pred. No. 5.2e-20;
Matches 76; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

QY 1 MAGELTPEEEAQQKAFSAVDGTGNGTINAQELGAALKATGKNLSAQLRKLISEVDSG 60
DB 1 MADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTAEALQDMINEVDAG 60
QY 61 DGEISFOEFLT-AARKAR--AGLEDLOVAFRAFDODGDGHITVDLRRAMAGLQPLPOE 117
DB 61 NGTIDFPEELTMMARKMKTDSEEEIREAFRVFDKDGNGFISAAELRHVYMTNLGEKLTDE 120
QY 118 ELDAMIREADVDDQGRVNYEEFARMIAQE 146
DB 121 EVDEMIREADIDGCGQVNYEEFVMTWSK 149

Search completed: March 24, 2003, 17:45:37
Job time : 19 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 17:43:25 ; Search time 12 Seconds
(without alignments)
504.629 Million cell updates/sec

Title: US-10-031-403-1

Perfect score: 729

Sequence: 1 MAGELTPEEAQYKARSAV.....DVQDGRVNYEFPARMLAQE 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	729	100.0	146	1	CLSP_HUMAN	Q9nzt1	homo sapien
2	388.5	53.3	148	1	CALM_METSE	P02596	metridium s
3	388.5	53.3	149	1	CALM_PLAFA	P24044	plasmodium
4	385.5	52.9	148	1	CALM_FATSP	P20595	patinopecte
5	380.5	52.2	148	1	CALM_PYUSP	P11121	pyuridae sp
6	379.5	52.1	148	1	CALM_HUMAN	P02593	homo sapien
7	378.5	51.9	148	1	CALM_STIJA	P21251	stichopus j
8	377.5	51.8	148	1	CALM_ELEEL	P02594	electrophor
9	375.5	51.5	148	1	CALM_DROME	P07181	drosofila
10	371	50.9	148	1	CLM4_MOUSE	Q9jms3	mus musculus
11	369.5	50.7	148	1	CALM_PHYIN	P27165	phytophthor
12	369.5	50.7	162	1	CALM_CHLRE	P04352	chlamydomon
13	368.5	50.5	148	1	CALM_BLAEM	Q9hfy6	blastoclad
14	368.5	50.5	148	1	CALM_PLEOS	O94739	pleurotus o
15	367.5	50.4	148	1	CALM_PLECO	P11120	pleurotus c
16	366.5	50.3	148	1	CALM_TRYCR	P18061	trypanosoma
17	365.5	50.1	148	1	CALM_STYLE	P27166	stylonychia
18	365.5	50.1	148	1	CALM_TETPY	P02598	tetrahymena
19	365.5	50.1	148	1	CALM_TRYBB	P04465	trypanosoma
20	364.5	50.0	148	1	CALM_EUGGR	P11118	euglena gra
21	364.5	50.0	155	1	CALF_NAEGR	P53440	naegleria g
22	362.5	49.7	148	1	CALM_FARTE	P07463	paramecium
23	361.5	49.6	151	1	CALM_DICDI	P02599	dictyosteli
24	360.5	49.5	148	1	CALM_ACHKL	P15094	achlya kleb
25	358.5	49.2	148	1	CALS_CHICK	P02597	gallus gall
26	357.5	49.0	148	1	CALM_SPIOI	P04353	spinacia ol
27	355.5	48.8	138	1	CALL_ARBPV	P05932	arabacia pun
28	354.5	48.6	148	1	CALM_LYCES	P27161	lycopersico
29	354	48.6	149	1	CALM_WHEAT	P04464	tritium ae
30	353.5	48.5	148	1	CALM_HORVU	P13565	hordeum vul
31	353.5	48.5	148	1	CALM_MEDSA	P17928	medicago sa
32	353.5	48.5	148	1	CALM_ORYSA	P29612	oryza sativ
33	352.5	48.4	148	1	CALL_HUMAN	P27482	homo sapien

34	350.5	48.1	148	1	CALL_PETHY	P27162	petunia hyb
35	350.5	48.1	148	1	CAL6_ARATH	Q03509	arabidopsis
36	350.5	48.1	148	1	CALM_HELAN	P93171	heliathanus
37	350.5	48.1	148	1	CALM_MAIZE	P41040	zea mays (m
38	350.5	48.1	148	1	CALM_SOLTU	P13868	solanum tub
39	350.5	48.1	183	1	CAL3_PETHY	P27164	petunia hyb
40	349.5	47.9	148	1	CAL2_PETHY	P27163	petunia hyb
41	347.5	47.7	148	1	CAL2_ARATH	P25069	arabidopsis
42	347.5	47.7	148	1	CALM_CAPAN	P93087	capsicum an
43	344.5	47.3	131	1	CALN_CHICK	P05419	gallus gall
44	342.5	47.0	148	1	CAL4_ARATH	Q03510	arabidopsis
45	340.5	46.7	148	1	CALM_EMENI	P19533	emericalia

ALIGNMENTS

RESULT 1

ID	CLSP_HUMAN	STANDARD;	PRT;	146 AA.
AC	Q9N2T1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Calmodulin-like skin protein.			
GN	CLSP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Skin;			
RC	MEDLINE=20239936; PubMed=10777582;			
RA	Mehul B., Bernard D., Simonetti L., Bernard M.A., Schmidt R.;			
RT	Identification and cloning of a new calmodulin-like protein from human epidermis.			
RL	J. Biol. Chem. 275:12841-12847(2000).			
CC	-!- FUNCTION: BINDS CALCIUM. MAY BE INVOLVED IN TERMINAL DIFFERENTIATION OF KERATINOCYTES.			
CC	-!- SUBUNIT: ASSOCIATES WITH TRANSLUTAMINASE 3.			
CC	-!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN THE EPIDERMIS WHERE ITS EXPRESSION IS DIRECTLY RELATED TO KERATINOCYTE DIFFERENTIATION. VERY LOW EXPRESSION IN LUNG.			
CC	-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; AF172852; AAF66821.1; --			
DR	HSSP; P02593; IFW4.			
DR	MIM; 605183; --			
DR	InterPro; IPR002048; EF-hand.			
DR	Pfam; PF00036; ehand; 4.			
DR	ProDom; PD000012; EF-hand; 2.			
DR	SMART; SM00054; EFh; 4.			
DR	PROSITE; PS00018; EF-HAND; 4.			
KW	Calcium-binding; Repeat.			
FT	CA_BIND 21..32			EF-HAND 1 (POTENTIAL).
FT	CA_BIND 57..68			EF-HAND 2 (POTENTIAL).
FT	CA_BIND 91..102			EF-HAND 3 (POTENTIAL).
FT	CA_BIND 127..138			EF-HAND 4 (POTENTIAL).
SQ	SEQUENCE 146 AA; 15920 MW; 6F565F8E04B994CC CRC64;			

Query Match 100.0%; Score 729; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGELTPEEAQYKAFSAVDGNGTINAOELGAALKATGKNLSEAQLKLISEVSDG 60
 Db 1 MAGELTPEEAQYKAFSAVDGNGTINAOELGAALKATGKNLSEAQLKLISEVSDG 60
 QY 61 DGEISFQEFLLTAARKARAGLEDLVAFRAFDQDGDGHITVDELRRAMAGLQPLPOEELD 120
 Db 61 DGEISFQEFLLTAARKARAGLEDLVAFRAFDQDGDGHITVDELRRAMAGLQPLPOEELD 120
 QY 121 AMIREADVDDQGRVNYEEFARMQAQ 146
 Db 121 AMIREADVDDQGRVNYEEFARMQAQ 146

RESULT 2
 CALM_METSE STANDARD; PRT; 148 AA.
 AC P02596;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 01, Last annotation update)
 DE Calmodulin.
 OS Metridium senille (Brown sea anemone) (Frilled sea anemone), and
 OS Renilla reniformis (Sea pansy).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyanthaeae; Metridiidae; Metridium.
 OX NCBI_TaxID=6116, 6136;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81062446; PubMed=6108109;
 RA Takagi T., Nemoto T., Konishi K., Yazawa M., Yagi K.;
 FT "The amino acid sequence of the calmodulin obtained from sea anemone
 RT (metridium senille) muscle.";
 RL Biochem. Biophys. Res. Commun. 96:377-381(1980).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=81205529; PubMed=6263143;
 RA Jamieson G.A. Jr., Bronson D.D., Schachat F.H., Vanaman T.C.;
 FT "Structure and function relationships among calmodulins and troponin
 RT C-like proteins from divergent eukaryotic organisms.";
 RL Ann. N.Y. Acad. Sci. 356:1-13(1980).
 CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
 CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
 CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
 CC PHOSPHATASES.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 DR PIR; A90223; MCXAM.
 DR HSP; A90036; MCJZR.
 DR HSP; P02593; IAK8.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 4.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR Calcium-binding; Repeat; Methylation.
 KW MOD_RES 1 1 BLOCKED.
 FT MOD_RES 115 115 METHYLATION (TRI-).
 FT CA_BIND 20 31 EF-HAND 1.
 FT CA_BIND 56 67 EF-HAND 2.
 FT CA_BIND 93 104 EF-HAND 3.
 FT CA_BIND 129 140 EF-HAND 4.
 SQ SEQUENCE 148 AA; 16708 MW; 4CEE8EBC4D750AA CRC64;

Query Match 53.3%; Score 388.5; DB 1; Length 148;
 Best Local Similarity 52.0%; Pred. No. 7.3e-19;
 Matches 77; Conservative 30; Mismatches 38; Indels 3; Gaps 2;

QY 2 AGEITPEEAQYKAFSAVDGNGTINAOELGAALKATGKNLSEAQLKLISEVSDG 61
 Db 1 ADQLEEQIAEFKAFSLDFKDGDTITTKELGTVMRSLGQNPTEAEALQDMINEVDADG 60
 QY 62 GEISFQEFLLTAARKAR--AGLEDLVAFRAFDQDGDGHITVDELRRAMAGLQPLPOEE 118

Db 61 GTIDFPEELTMMARKMDTDEEEIREAFRVFDKDGDFISAAELRHVMTNLGKLTDEE 120
 QY 119 LDAMIREADVDDQGRVNYEEFARMQAQ 146
 Db 121 VDEMIREADVDDQGRVNYEEFARMQAQ 148

RESULT 3
 CALM_PLAFA STANDARD; PRT; 149 AA.
 AC P24044;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calmodulin.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ISolate FC27;
 RX MEDLINE=92008475; PubMed=1915742;
 RA Cowman A.F., Galatis D.;
 FT "Plasmodium falciparum: the calmodulin gene is not amplified or
 RT overexpressed in chloroquine resistant or sensitive isolates.";
 RL Exp. Parasitol. 73:269-275(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91304518; PubMed=1852174;
 RA Robson K.J.H., Jennings M.W.;
 FT "The structure of the calmodulin gene of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 46:19-34(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93376007; PubMed=8366883;
 RA Robson K.J.H.;
 FT "Sequence diversity in the intron of the calmodulin gene from
 RT Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 60:1-8(1993).
 CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
 CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
 CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
 CC PHOSPHATASES.
 CC -1- MISCELLANEOUS: CALMODULIN IS NOT INVOLVED IN THE MECHANISM OF
 CC CHLOROQUINE RESISTANCE.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; M59349; AAA29509.1; -;
 DR EMBL; X56950; CAA40264.1; -;
 DR EMBL; M59770; AAA29510.1; -;
 DR EMBL; M99442; AAA29508.1; -;
 DR PIR; S21813; S21813.
 DR PIR; B45594; B45594.
 DR PIR; A49774; A49774.
 DR HSP; P02593; ICDM.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 4.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR Calcium-binding.
 FT CA_BIND 21 32 EF-HAND 1.
 FT CA_BIND 57 68 EF-HAND 2.
 FT CA_BIND 94 105 EF-HAND 3.


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FT CA_BIND 130 141 EF-HAND 4.
FT CONFLICT 28 30 MISSING (IN REF. 1).
SQ SEQUENCE 149 AA; 16931 MW; 30D806FDA2BC173 CRC64;

Query Match 53.3%; Score 388.5; DB 1; Length 149;
Best Local Similarity 52.1%; Pred. No. 7.3e-19;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

-QY 1 MAGELTPEEAQYKFAFSAVDTDGNGTINAEALGALKATGKNLSEALRKLISEVDSGD 60
DQ 1 MADKLTEQISEKFAFSLFDKDGDTITTKELGTVMRSLGQNPTEAEIQMINEIDTDG 60
QY 61 DGEISFQELT-AARKAR--AGLEDLOVAFRAFDGDDGHITVDELRRAMAGIGQPLPOE 117
DQ 61 NGTIDPFELTMAKLKDTDETELEAEAFRVFDKDGDIYSADELHRVMTNLGEKLTNE 120
QY 118 ELAMIREADVDQGRVNYEEFARM 143
DQ 118 ELAMIREADVDQGRVNYEEFARM 143
DQ 121 EVDEMIREADIDGQVNYEEFVMTSK 146

RESULT 4
CALM_PATSP STANDARD; PRT; 148 AA.
AC P02595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Patinopecten sp. (Scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Patinopecten.
OX NCBI_TaxID=6574;
RN [1]
RP SEQUENCE.
RX MEDLINE=82167261; PubMed=7338518;
RA Toda H., Yazawa M., Kondo K., Honma T., Narita K., Yagi K.;
RT "Amino acid sequence of calmodulin from scallop (Patinopecten)
RT adductor muscle.";
RL J. Biochem. 90:1493-1505(1981).
CC -|- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -|- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -|- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR PIR; A03023; MCSW.
DR HSP; P07181; 4CLN.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
SQ SEQUENCE 148 AA; 16681 MW; 4CEEBE8C4C5C0A CRC64;

Query Match 52.9%; Score 385.5; DB 1; Length 148;
Best Local Similarity 52.0%; Pred. No. 1.1e-18;
Matches 77; Conservative 29; Mismatches 39; Indels 3; Gaps 2;

-QY 2 AGELTPEEAQYKFAFSAVDTDGNGTINAEALGALKATGKNLSEALRKLISEVDSGD 61
DQ 1 ADQLTEQIAEFKFAFSLFDKDGDTITTKELGTVMRSLGQNPTEAEIQMINEVDAGD 60
QY 62 GEISFQELT-AARKAR--AGLEDLOVAFRAFDGDDGHITVDELRRAMAGIGQPLPOE 118
DQ 61 GTIDPFELTMMARKDTSDEEIREAFRVFDKDGDIYSADELHRVMTNLGEKLTDEE 120

RESULT 5
CALM_PYUSP STANDARD; PRT; 148 AA.
AC P11121;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Pyridae sp. (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyridae; unclassified Pyridae.
OX NCBI_TaxID=7734;
RN [1]
RP SEQUENCE.
RA Yazawa M., Toda H., Sakiyama F., Yagi K.;
RL Submitted (MAY-1988) to the PIR data bank.
CC -|- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -|- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -|- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR PIR; JK0015; MCAZS.
DR HSP; P07181; 4CLN.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Methylation; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT CA_BIND 115 115 METHYLATION.
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
SQ SEQUENCE 148 AA; 16680 MW; 4CEEBE57FA87BCA CRC64;

Query Match 52.2%; Score 380.5; DB 1; Length 148;
Best Local Similarity 51.4%; Pred. No. 2.4e-18;
Matches 76; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

-QY 2 AGELTPEEAQYKFAFSAVDTDGNGTINAEALGALKATGKNLSEALRKLISEVDSGD 61
DQ 1 ADQLTEQIAEFKFAFSLFDKDGDTITTKELGTVMRSLGQNPTEAEIQMINEVDAGD 60
QY 62 GEISFQELT-AARKAR--AGLEDLOVAFRAFDGDDGHITVDELRRAMAGIGQPLPOE 118
DQ 61 GTIDPFELTMMARKDTSDEEIREAFRVFDKDGDIYSADELHRVMTNLGEKLTDEE 120

RESULT 6
CALM_HUMAN STANDARD; PRT; 148 AA.
AC P02593; P90014; P70667; Q61379; Q61380;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
GN (CALM1 OR CAM1 OR CAM OR CAM) AND (CALM2 OR CAM2 OR CAMB) AND
GN (CALM3 OR CAM3 OR CAMC).
OS Homo sapiens (Human),

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OS Mus musculus (Mouse).
OS Rattus norvegicus (Rat).
OS Oryctolagus cuniculus (Rabbit).
OS Bos taurus (Bovine).
OS Gallus gallus (Chicken).
OS Anas platyrhynchos (Domestic duck).
OS Xenopus laevis (African clawed frog).
OS Arctia punctulata (Punctate sea urchin).
OS Oncorhynchus sp. (Salmon).
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI TaxID=9606, 10090, 10116, 9986, 9913, 9031, 8839, 8355, 7641,
OX 8025, 8090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE=89034207; PubMed=3182832;
RA Fischer R., Koller M., Flura M., Mathews S., Strehler-Pagge M.A.,
RA Krebs J., Penniston J.T., Carafoli E., Strehler E.E.;
RT "Multiple divergent mRNAs code for a single human calmodulin.";
RN J. Biol. Chem. 263:17055-17062(1988).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE=88059053; PubMed=2445749;
RA Sengupta B., Friedberg F., Detera-Wadleigh S.D.;
RT "Molecular analysis of human and rat calmodulin complementary DNA
clones. Evidence for additional active genes in these species.";
RN J. Biol. Chem. 262:16663-16670(1987).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE=85022688; PubMed=6385987;
RA Wawrzynczak E.J., Perham R.N.;
RT "Isolation and nucleotide sequence of a cDNA encoding human
calmodulin.";
RN Biochem. Int. 9:177-185(1984).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE=95010144; PubMed=7925473;
RA Rhyner J.A., Ottiger M., Wicki R., Greenwood T.M., Strehler E.E.;
RT "Structure of the human CALM1 calmodulin gene and identification of
two CALM1-related pseudogenes CALM1P1 and CALM1P2.";
RN Eur. J. Biochem. 225:71-82(1994).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES-Human; TISSUE=Lymphoma;
RA Kato S.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE.
RC SPECIES-Human; TISSUE=Brain;
RX MEDLINE=82231946; PubMed=7093203;
RA Sasagawa T., Ericsson L.H., Walsh K.A., Schreiber W.E., Fischer E.H.,
RA Titani K.;
RT "Complete amino acid sequence of human brain calmodulin.";
RN Biochemistry 21:2565-2569(1982).
[7]
RP SEQUENCE.
RC SPECIES-Rabbit; TISSUE=Skeletal muscle;
RX MEDLINE=81138220; PubMed=7202416;
RA Grand R.J.A., Shenolikar S., Cohen P.;
RT "The amino acid sequence of the delta subunit (calmodulin) of rabbit
skeletal muscle phosphorylase kinase.";
RN Eur. J. Biochem. 113:359-367(1981).
[8]
RP SEQUENCE.
RC SPECIES-Bovine; TISSUE=Brain;
RA Kasai H., Kato Y., Isobe T., Kawasaki H., Okuyama T.;
RT "Determination of the complete amino acid sequence of calmodulin
(phenylalanine-rich acidic protein II) from bovine brain.";
RN [9]
RP SEQUENCE.
RC SPECIES-Bovine; TISSUE=Brain;
RX MEDLINE=80094551; PubMed=7356670;
RA Watterson D.M., Sharief F., Vanaman T.C.;
RT "The complete amino acid sequence of the Ca2+-dependent modulator
protein (calmodulin) of bovine brain.";
RN J. Biol. Chem. 255:962-975(1980).
[10]
RP SEQUENCE.
RC SPECIES-Bovine; TISSUE=Uterus;
RA Grand R.J.A., Perry S.V.;
RT "The amino acid sequence of the troponin C-like protein (modulator
protein) from bovine uterus.";
RN FEBS Lett. 92:137-142(1978).
[11]
RP SEQUENCE OF 38-60.
RC SPECIES-Bovine;
RX MEDLINE=89064822; PubMed=3058479;
RA Pribilla I., Krueger H., Buchner K., Otto H., Schiebler W.,
RA Tripipler D., Hucho F.;
RT "Heat-resistant inhibitors of protein kinase C from bovine brain.";
RN Eur. J. Biochem. 177:657-664(1988).
[12]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RX MEDLINE=88257100; PubMed=3384819;
RA Bender P.K., Dedman J.R., Emerson C.P.;
RT "The abundance of calmodulin mRNAs is regulated in phosphorylase
kinase-deficient skeletal muscle.";
RN J. Biol. Chem. 263:9733-9737(1988).
[13]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RX MEDLINE=90006775; PubMed=2551780;
RA Danchin A., Sezer O., Glaser P., Chalou P., Caput D.;
RT "Cloning and expression of mouse-brain calmodulin as an activator of
Bordetella pertussis adenylate cyclase in Escherichia coli.";
RN Gene 80:145-149(1989).
[14]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Kato K.;
RT "A collection of cDNA clones with specific expression patterns in
mouse brain.";
RN Eur. J. Neurosci. 2:704-711(1991).
[15]
RP SEQUENCE.
RC SPECIES-Rat; TISSUE=Testis;
RX MEDLINE=78066877; PubMed=201628;
RA Dedman J.R., Jackson R.L., Schreiber W.E., Means A.R.;
RT "Sequence homology of the Ca2+-dependent regulator of cyclic
nucleotide phosphodiesterase from rat testis with other Ca2+-binding
proteins.";
RN J. Biol. Chem. 253:343-346(1978).
[16]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE=Brain;
RX MEDLINE=87246077; PubMed=2885164;
RA Sherbany A.A., Parent A.S., Brosius J.;
RT "Rat calmodulin cDNA.";
RN DNA 6:267-272(1987).
[17]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE=Brain;
RX MEDLINE=8726204; PubMed=3035194;
RA Nojima H., Hirofumi S.;
RT "Structure of a gene for rat calmodulin.";
RN J. Mol. Biol. 193:439-445(1987).
[18]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat;

```

RX MEDLINE=87257889; PubMed=3037336;
RA Nojima H., Kishi K., Sorabe H.;
RT "Multiple calmodulin mRNA species are derived from two distinct
RL genes.";
RL Mol. Cell. Biol. 7:1873-1880(1987).
RN [19]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-SHR;
RX MEDLINE=89362474; PubMed=2527998;
RA Nojima H.;
RT "Structural organization of multiple rat calmodulin genes.";
RL J. Mol. Biol. 208:269-282(1989).
RN [20]
RP SEQUENCE FROM N.A.
RC SPECIES-Chicken;
RX MEDLINE=84008199; PubMed=6137485;
RA Putkey J.A., Ts'ui K.F., Tanaka T., Lagace L., Stein J.P., Lai E.C.,
RT Means A.R.;
RT "Chicken calmodulin genes. A species comparison of cDNA sequences and
RT isolation of a genomic clone.";
RL J. Biol. Chem. 258:11864-11870(1983).
RN [21]
RP SEQUENCE FROM N.A.
RC SPECIES-Chicken;
RX MEDLINE=85104969; PubMed=2981850;
RA Simmen R.C.M., Tanaka T., Ts'ui K.F., Putkey J.A., Scott M.J.,
RA Lai E.C., Means A.R.;
RT "The structural organization of the chicken calmodulin gene.";
RL J. Biol. Chem. 260:907-912(1985).
RN [22]
RP ERRATUM.
RC SPECIES-Chicken;
RA Simmen R.C.M., Tanaka T., Ts'ui K.F., Putkey J.A., Scott M.J.,
RA Lai E.C., Means A.R.;
RL J. Biol. Chem. 262:4928-4929(1987).
RN [23]
RP SEQUENCE FROM N.A.
RC SPECIES-Chicken;
RA Iida Y.;
RT "cDNA sequences and molecular evolution of calmodulin genes of
RT chicken and eel.";
RL Bull. Chem. Soc. Jpn. 57:2667-2668(1984).
RN [24]
RP SEQUENCE FROM N.A.
RC SPECIES-A.platyrrhinos;

Query Match 52.1%; Score 379.5; DB 1; Length 148;
Best Local Similarity 51.7%; Pred. No. 2.7e-18;
Matches 75; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

QY 2 AGELTPEEAQYKKAFAVDGNGTINAQELGAALKATGKNLSEAQLRLKLISEVDSGD 61
DB 1 ADQLTEQIAEFAEFSLFDKDGDTITTKELGTVMRSLGNPTAEALQDMINEVDADGN 60
QY 62 GEISFQEFLLT-AARKAR--AGLEDLQVAFRAFDQGDGHITVDELRRAMAGLQGPLQEE 118
DB 61 GTIDFPEFLTMARKMKDTSDEEIRAFRFDKNGYISAAELRHVMTNLGKLTDEE 120
QY 119 LDAMIREADVDDGRVNYEEFARM 143
DB 121 VDEMIREADIDGQVNYEEFVQMM 145

RESULT 7
CALM.STIJA
ID CALM.STIJA STANDARD; PRT; 148 AA.
AC F21251;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Stichopus japonicus (Sea cucumber).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Query Match 51.9%; Score 378.5; DB 1; Length 148;
Best Local Similarity 50.7%; Pred. No. 3.2e-18;
Matches 75; Conservative 32; Mismatches 38; Indels 3; Gaps 2;

QY 2 AGELTPEEAQYKKAFAVDGNGTINAQELGAALKATGKNLSEAQLRLKLISEVDSGD 61
DB 1 ADQLTEQIAEFAEFSLFDKDGDTITTKELGTVMRSLGNPTAEALQDMINEVDADGN 60
QY 62 GEISFQEFLLT-AARKAR--AGLEDLQVAFRAFDQGDGHITVDELRRAMAGLQGPLQEE 118
DB 61 GTIDFPEFLTMARKMKDTSDEEIRAFRFDKNGYISAAELRHVMTNLGKLTDEE 120
QY 119 LDAMIREADVDDGRVNYEEFARM 146
DB 121 VDEMIREADIDGQVNYEEFVMTSK 148

RESULT 8
CALM.ELEEL
ID CALM.ELEEL STANDARD; PRT; 148 AA.
AC P02594; Q90496;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Electroplax;
RX MEDLINE=83108962; PubMed=6185488;
RA Lagace L., Chandra T., Woo S.L.C., Means A.R.;
RT "Identification of multiple species of calmodulin messenger RNA using
RT a full length complementary DNA.";
RL J. Biol. Chem. 258:1684-1688(1983).
RN [2]
RP SEQUENCE FROM N.A.

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OC Holothuroidea; Aspidochirotea; Aspidochirotida; Stichopodidae;
OC Stichopus.
OX NCBI_TaxID=7692;
RN [1]
RP SEQUENCE.
RA Toda H., Abe Y., Yazawa M., Yagi K.;
RT "Amino acid sequence of sea cucumber calmodulin.";
RL Seikagaku 57:1037-1037(1985).
CC -I- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -I- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR PIR; JK0011; MGSFCU.
DR HSSP; P02593; LAK8.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Methylation.
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 115 115 METHYLATION.
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
FT VARIANT 78 78 D -> E.
FT VARIANT 99 99 Y -> F.
SQ SEQUENCE 148 AA; 16695 MW; 4653EA287472DICA CRC64;

Query Match 51.9%; Score 378.5; DB 1; Length 148;
Best Local Similarity 50.7%; Pred. No. 3.2e-18;
Matches 75; Conservative 32; Mismatches 38; Indels 3; Gaps 2;

QY 2 AGELTPEEAQYKKAFAVDGNGTINAQELGAALKATGKNLSEAQLRLKLISEVDSGD 61
DB 1 ADQLTEQIAEFAEFSLFDKDGDTITTKELGTVMRSLGNPTAEALQDMINEVDADGN 60
QY 62 GEISFQEFLLT-AARKAR--AGLEDLQVAFRAFDQGDGHITVDELRRAMAGLQGPLQEE 118
DB 61 GTIDFPEFLTMARKMKDTSDEEIRAFRFDKNGYISAAELRHVMTNLGKLTDEE 120
QY 119 LDAMIREADVDDGRVNYEEFARM 146
DB 121 VDEMIREADIDGQVNYEEFVMTSK 148

RESULT 8
CALM.ELEEL
ID CALM.ELEEL STANDARD; PRT; 148 AA.
AC P02594; Q90496;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Electroplax;
RX MEDLINE=83108962; PubMed=6185488;
RA Lagace L., Chandra T., Woo S.L.C., Means A.R.;
RT "Identification of multiple species of calmodulin messenger RNA using
RT a full length complementary DNA.";
RL J. Biol. Chem. 258:1684-1688(1983).
RN [2]
RP SEQUENCE FROM N.A.

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Viskas R., Rector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [5]
RN SEQUENCE OF 1-140 FROM N.A.
RP SPECIES=D.melanogaster;
RC MEDLINE=87228266; PubMed=3035324;
RX Beckingham K., Doyle K.E., Maune J.F.;
RA "The calmodulin gene of *Drosophila melanogaster*.";
RL Meth. Enzymol. 139:230-247(1987).
RN [6]
RN SEQUENCE
RP SPECIES=L.migratoria;
RC Toda H.;
RA Submitted (MAY-1988) to the PIR data bank.
RN [7]
RN SEQUENCE FROM N.A.
RP SPECIES=A.californica; TISSUE=Ganglion;
RX MEDLINE=91080147; PubMed=2258931;
RA Swanson M.E., Sturmer S.F., Schwartz J.H.;
RT "Structure and expression of the *Aplysia californica* calmodulin
RT gene.";
RL J. Mol. Biol. 216:545-553(1990).
RN [8]
RN SEQUENCE FROM N.A.
RP SPECIES=B.floridiae;
RC Karabinos A., Riener D., Weber K.;
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RN SEQUENCE FROM N.A.
RP SPECIES=H.toretzi;
RC MEDLINE=99196995; PubMed=10095116;
RX Yuasa H.J., Yamamoto H., Takagi T.;
RA "The structural organization of the ascidian, *Halocynthia roretzi*,
RT calmodulin genes.";
RT calmodulin genes.";
RL Gene 229:163-169(1999).
RN [10]
RN SEQUENCE FROM N.A.
RP SPECIES=H.toretzi, B.floridiae, and B.lanceolatum;
RC Yuasa H.J., Takagi T.;
RA "Primary structure of Protochordate calmodulin.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [11]
RN STRUCTURE BY NMR.
RP SPECIES=D.melanogaster;
RC MEDLINE=91369934; PubMed=1909892;
RX Ikura M., Spera S., Barbato G., Kay L.E., Krinks M., Bax A.;
RA "Secondary structure and side-chain 1H and 13C resonance assignments
RT of calmodulin in solution by heteronuclear multidimensional NMR
RT spectroscopy.";
RL Biochemistry 30:9216-9228(1991).
RN [12]
RN STRUCTURE BY NMR.
RP SPECIES=D.melanogaster;
RC MEDLINE=92263094; PubMed=1585175;
RX Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
RA "Solution structure of a calmodulin-target peptide complex by
RT multidimensional NMR.";
RL Science 256:632-638(1992).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP SPECIES=D.melanogaster;
RC MEDLINE=92042027; PubMed=1939171;
RX Taylor D.A., Sack J.S., Maune J.F., Beckingham K., Quirocho F.A.;
RA "Structure of a recombinant calmodulin from *Drosophila melanogaster*
RT refined at 2.2-A resolution.";

RL J. Biol. Chem. 266:21375-21380(1991).
CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00133; CAA68327.1; -;
DR EMBL; X05948; CAA29380.1; -;
DR EMBL; X05949; CAA29381.1; -;
DR EMBL; X05950; CAB51566.1; -;
DR EMBL; X05951; CAA29383.1; -;
DR EMBL; AE003823; AAF58542.1; -;
DR EMBL; AE003823; AAF58543.1; -;
DR EMBL; X56888; CAA40207.1; -;
DR EMBL; X54653; -; NOT_ANNOTATED_CDS.
DR EMBL; X54655; -; NOT_ANNOTATED_CDS.
DR EMBL; Y09863; CAA70990.1; -;
DR EMBL; Y09880; CAA71006.1; -;
DR EMBL; AB018796; BAA33967.1; -;
DR EMBL; AB003081; BAA19786.1; -;
DR EMBL; AB003082; BAA19787.1; -;
DR EMBL; AB003083; BAA19788.1; -;
DR PIR; JK0010; MCLQ.
DR PIR; S01173; MCGF.
DR PIR; S13248; MCGAC.
DR PDB; 4CLN; 15-JUL-92.
DR PDB; 2BBW; 31-JAN-94.
DR PDB; 2BBN; 31-JAN-94.
DR FlyBase; FBgn0000253; Cam.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Methylation; 3D-structure.
FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED (IN LOCUST).
FT MOD_RES 115 115 METHYLATION (IN LOCUST).
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
Query Match 51.5%; Score 375.5; DB 1; Length 148;
Best Local Similarity 50.7%; Pred. No. 4.9e-18;
Matches 75; Conservative 31; Mismatches 39; Indels 3; Gaps 2;
QY 2 AGELTPPEEAQYKKAFAVDGDTGNGTINAOALGATKATGNLSEAOLKLTSEVDSGDG 61
Db 1 ADQLTEEQIAEFKEAFSLFDKDGDTTTELGTVMRSLGQNPTEAELODMINEVDADGN 60
QY 62 GEISFQEFELT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDLRRMAGLGPPLPOEE 118
Db 61 GTIDFPEFLTMARKMDTDEEIREAFRVFDKDGNGFISAAELRHVMTNLGKLTDEE 120
QY 119 LDAMIRADVDDQGRVNYEEFARMQAQE 146
Db 121 VDEMIREADIDGCGQVNYEEFVTMTSK 148
RESULT 10
CLM4_MOUSE

CLM4_MOUSE STANDARD; PRT; 148 AA.
Q9UM83; Q9CR31; Q9DIE9;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin 4 (Calcium-binding protein Ddl12).
GN CALM4 OR Ddl12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikegawa S., Nakamura Y.;
RT Ddl12, a novel mouse gene implicated in the early stage of ectopic
RT ossification.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Stauber L., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: IMPLICATED IN THE EARLY STAGE OF ECTOPIC OSSIFICATION.
CC -1- SIMILARITY: CONTAINS 3 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC
CC EMBL; AB036744; BAA95412.1; -
DR EMBL; AK009956; BAB26608.1; -
DR EMBL; AK009664; BAB26425.1; -
DR EMBL; AK003648; BAB22914.1; -
DR HSSP; P02593; 1CDM.
DR MGD; MGI:1931464; Calm4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF000036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 3.
KW Calcium-binding; Repeat.
FT CA_BIND 21 32 EF-HAND 1 (POTENTIAL).
FT CA_BIND 57 68 EF-HAND 2 (POTENTIAL).
FT CA_BIND 93 104 EF-HAND 3 (POTENTIAL).
FT CONFLICT 9 9 E -> V (IN REF. 2; BAB22914).
FT CONFLICT 124 124 M -> V (IN REF. 2; BAB22914).
FT CONFLICT 146 148 VEN -> I (IN REF. 1).
SQ SEQUENCE 148 AA; 16767 MW; 2AE22BC738AD2F9D CRC64;

Query Match 50.9%; Score 371; DB 1; Length 148;
Best Local Similarity 51.4%; Pred. No. 9.5e-18;
Matches 74; Conservative 29; Mismatches 39; Indels 2; Gaps 1;
Qy 1 MAGELTPEEAQYKFAKFAVTDGNGTTNAQELGAALAKATKKNLSEAQLKLISEVSDSG 60
Db 1 MSHGFTKEEVAEFAQAFNRFDKNKGHSIVELGDMVKQLGNLPEKDLKALISLDTDG 60
Qy 61 DGEISFQFLFAARKARAG--LEDQVAFRAFDQDGDGHITVDELRRAAGLQGPLPOEE 118
Db 61 DGKISFEFLFAIEKYKKGHRAGELRAVFNLDQNGDGTITVDELKESLKLGSLSQEE 120
Qy 119 LDAMIREADVDDQGRVNYEEFARM 142
Db 121 LEDMIRVADVDDQGRVNYEEFARM 144
RESULT 11
CALM_PHYIN STANDARD; PRT; 148 AA.
AC P27165;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin (CaM).
GN CMD1 OR CALP1.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=932229802; PubMed=8471792;
RA Pieterse C.M., Verbakel H.M., Spaans J.H., Davide L.C., Govers F.;
RT "Increased expression of the calmodulin gene of the late blight
RT fungus Phytophthora infestans during pathogenesis on potato.";
RL Mol. Plant Microbe Interact. 6:164-172(1993).
CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M83535; AAA21424.1; -
DR HSSP; P02593; IAK8.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF000036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT INIT_MET 0 0 BY SIMILARITY.
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
SQ SEQUENCE 148 AA; 16693 MW; 5F7F7EDFCD0A46D4 CRC64;
Query Match 50.7%; Score 369.5; DB 1; Length 148;
Best Local Similarity 50.3%; Pred. No. 1.2e-17;
Matches 73; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

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QY 2 AGELTPEEAQYKARSAVDGNGTINAGELGAALKATGKLNLSAQLRKLISEVDSGD 61
Db 1 ADQLEEQIAEFKEAFSLFDKGGDTTITTKELGTVMRSLGQNPTEAELODMINEVDAGN 60
QY 62 GEISFQEFIT-AARKAR--AGLEDQVAFRAFDQDGHITVDLRRAMAGLGOPLPOEE 118
Db 61 GTIDFPEFLTMARKMKDTSSEIELEAFKFDKNGGNGFISAAELRHINTNLSEKLTDEE 120
QY 119 LDAMIREADVDDGRVNYEEFARM 143
Db 121 VDEMIREADIDGGOINYEFEVRMM 145

RESULT 12
CALM_CHLRE STANDARD; PRT; 162 AA.
AC P04352;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89066752; PubMed=3198631;
RA Zimmer W.E., Schloss J.A., Silflow C.D., Youngblom J., Watterson D.M.;
RT "Structural organization, DNA sequence, and expression of the
calmodulin gene";
RL J. Biol. Chem. 263:19370-19383(1988).
RN [2]
RP SEQUENCE.
RA Lukus T.J., Wiggins M.E., Watterson D.M.;
RT "Amino acid sequence of a novel calmodulin from the unicellular alga
Chlamydomonas";
RL Plant Physiol. 78:477-483(1985).
CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
PHOSPHATASES.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES.
CC -1- MISCELLANEOUS: METHYLATION STATE OF K-118 MAY BE IMPORTANT IN THE
QUANTITATIVE REGULATION OF PLANT NAD KINASE ACTIVITY. AMONG THE
EUKARYOTIC CALMODULINS, ONLY THE CHLAMYDOMONAS AND DICTYOSTELIUM
PROTEINS HAVE AN UNMETHYLATED LYSINE AT THIS POSITION, AND ONLY
THESE PROTEINS CAN INCREASE (4- TO 6-FOLD) THE MAXIMAL ACTIVATION
OF THIS ENZYME.
CC -1- MISCELLANEOUS: THIS PROTEIN IS UNUSUAL AMONG EUKARYOTIC
CALMODULINS IN HAVING AN 11-RESIDUE EXTENSION OF ITS CARBOXYL END.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
CC EMBL; M20729; AAA33083.1; -.
CC PIR; A03030; MCKM.
CC HSSP; P02593; MCKM.
CC InterPro: IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF_HAND; 4.
CC Calcium-binding; Repeat; Acetylation.
CC INIT_MET 0 0
CC MOD_RES 1 1 ACETYLATION.
CC FT

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FT CA_BIND 23 34 EF-HAND 1.
FT CA_BIND 59 70 EF-HAND 2.
FT CA_BIND 96 107 EF-HAND 3.
FT CA_BIND 132 143 EF-HAND 4.
SQ SEQUENCE 162 AA; 18165 MW; DD0779F5AE4AA7D2 CRC64;

Query Match 50.7%; Score 369.5; DB 1; Length 162;
Best Local Similarity 51.7%; Pred. No. 1.3e-17;
Matches 74; Conservative 31; Mismatches 35; Indels 3; Gaps 2;

QY 4 ELTPPEEAQYKARSAVDGNGTINAGELGAALKATGKLNLSAQLRKLISEVDSGDGE 63
Db 6 OLTEEQIAEFKEAFSLFDKGGDTTITTKELGTVMRSLGQNPTEAELODMISEVDAGNGT 65
QY 64 ISQEFEL-TAARKAR--GLEDLQVAFRAFDQDGHITVDLRRAMAGLGOPLPOBELD 120
Db 66 IDRPEFLMLARKMKETDHEDELREAFKFDKNGGNGFISAAELRHVMTNLGEKLSSEVD 125
QY 121 AMIREADVDDGRVNYEEFARM 143
Db 126 EMIREADVDDGGOVNYEEFVRMM 148

RESULT 13
CALM_BLAEM STANDARD; PRT; 148 AA.
AC Q9HFY6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin (Cam).
GN CMD1.
OS Blastocladiaella emersonii.
OC Eukaryota; Fungi; Chytridiomycota; Blastocladiaceae; Blastocladiaceae;
OC Blastocladiella.
OX NCBI_TaxID=4808;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21140061; PubMed=11244068;
RA Simao R.C.G., Gomes S.L.;
RT "Structure, expression, and functional analysis of the gene coding
for calmodulin in the chytridiomycete Blastocladiaella emersonii.";
RL J. Bacteriol. 183:2280-2288(2001).
CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
PHOSPHATASES (By similarity).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL; AF264065; AAG31446.1; -.
CC HSSP; P02593; IAK8.
CC InterPro: IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF_HAND; 4.
CC Calcium-binding; Repeat; Methylation.
CC INIT_MET 0 0 BY SIMILARITY.
CC MOD_RES 115 115 METHYLATION (BY SIMILARITY).
CC FT CA_BIND 20 31 EF-HAND 1.
CC FT CA_BIND 56 67 EF-HAND 2.
CC FT CA_BIND 93 104 EF-HAND 3.
CC FT CA_BIND 129 140 EF-HAND 4.

```


SQ SEQUENCE 148 AA; 16651 MW; 0887BFA32AD834B2 CRC64;

Query Match 50.5%; Score 368.5; DB 1; Length 148;
 Best Local Similarity 49.7%; Pred. No. 1.4e-17;
 Matches 72; Conservative 35; Mismatches 35; Indels 3; Gaps 2;

OY 2 AGELTPEEEAYKKAFSAVDTDGNGTINNAQELGAALKATGKNLSAQLRKLISEVDSGD 61
 DB 1 ADQLSEEQISEFKEAFSLFDKGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

OY 62 GEISFOEFLT-AARKAR--AGLEDQVAFRAFQDGDGHITVDELRRAAGLQGPLPOEE 118
 DB 61 GTIDFPEFLTMMARKMRDTSDEEIKFAKVFQDKDNGYISAAELRHVMTNLGKLTONE 120

OY 119 LDAMTREADVDQDGRVNYEEFARM 143
 DB 121 VEEMTREADVDGQINYEYFVKMM 145

RESULT 14
 CLM_PLEOS
 ID CLM_PLEOS STANDARD; PRT; 148 AA.
 AC 094739;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calmodulin (Cam).
 GN CML.
 OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Pleurotaceae; Pleurotus.
 OX NCBI_TaxID=5322;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park I., Yim J.;
 RT "Structure and sequence of the calmodulin gene from pleurotus
 ostreatus";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
 CC ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
 CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
 CC PHOSPHATASES (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC
 CC EMBL; U91642; AAD17455.1; -;
 CC EMBL; U91643; AAD17456.1; -;
 CC HSP; P02593; IAK8.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; efhand; 4.
 CC ProDom; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFh; 4.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC Calcium-binding; Repeat; Acetylation.
 CC INIT_MET 0 0 BY SIMILARITY.
 CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 CC FT CA_BIND 20 31 EF-HAND 1.
 CC FT CA_BIND 56 67 EF-HAND 2.
 CC FT CA_BIND 93 104 EF-HAND 3.
 CC FT CA_BIND 129 140 EF-HAND 4.
 CC SEQUENCE 148 AA; 16693 MW; CA5A2344770EF12C CRC64;

Query Match 50.5%; Score 368.5; DB 1; Length 148;
 Best Local Similarity 49.7%; Pred. No. 1.4e-17;

Matches 72; Conservative 34; Mismatches 36; Indels 3; Gaps 2;

OY 2 AGELTPEEEAYKKAFSAVDTDGNGTINNAQELGAALKATGKNLSAQLRKLISEVDSGD 61
 DB 1 ADQLSEEQISEFKEAFSLFDKGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

OY 62 GEISFOEFLT-AARKAR--AGLEDQVAFRAFQDGDGHITVDELRRAAGLQGPLPOEE 118
 DB 61 GTIDFPEFLTMMARKMRDTSDEEIKFAKVFQDKDNGYISAAELRHVMTNLGKLTONE 120

OY 119 LDAMTREADVDQDGRVNYEEFARM 143
 DB 121 VEEMTREADVDGQINYEYFVKMM 145

RESULT 15
 CALM_PLECO
 ID CALM_PLECO STANDARD; PRT; 148 AA.
 AC P11120;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calmodulin (Cam).
 GN CML.
 OS Pleurotus cornuoplae (Cornucopia mushroom).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Pleurotaceae; Pleurotus.
 OX NCBI_TaxID=5321;
 RN [1]
 RP SEQUENCE.
 RA Toda H., Sakiyama F., Yokono T., Miura K., Nakamura T.;
 RT "Amino acid sequence of Pleurotus cornuoplae calmodulin";
 RL Seikagaku 59:589-589(1987).
 CC -1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
 CC ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
 CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
 CC PHOSPHATASES.
 CC -1- PTM: UNLIKE OTHER CALMODULINS, LYS-115 IS NOT TRIMETHYLATED.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
 CC PIR; JK0014; MCMRP.
 CC HSP; P02593; IAK8.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; efhand; 4.
 CC ProDom; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFh; 4.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC Calcium-binding; Repeat; Acetylation.
 CC MOD_RES 1 1 ACETYLATION.
 CC FT CA_BIND 20 31 EF-HAND 1.
 CC FT CA_BIND 56 67 EF-HAND 2.
 CC FT CA_BIND 93 104 EF-HAND 3.
 CC FT CA_BIND 129 140 EF-HAND 4.
 CC SEQUENCE 148 AA; 16707 MW; CA5A3528A70EF12C CRC64;

Query Match 50.4%; Score 367.5; DB 1; Length 148;
 Best Local Similarity 49.0%; Pred. No. 1.6e-17;
 Matches 71; Conservative 35; Mismatches 36; Indels 3; Gaps 2;

OY 2 AGELTPEEEAYKKAFSAVDTDGNGTINNAQELGAALKATGKNLSAQLRKLISEVDSGD 61
 DB 1 ADQLSEEQISEFKEAFSLFDKGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

OY 62 GEISFOEFLT-AARKAR--AGLEDQVAFRAFQDGDGHITVDELRRAAGLQGPLPOEE 118
 DB 61 GTIDFPEFLTMMARKMRDTSDEEIKFAKVFQDKDNGYISAAELRHVMTNLGKLTONE 120

OY 119 LDAMTREADVDQDGRVNYEEFARM 143
 DB 121 VEEMTREADVDGQINYEYFVKMM 145

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us-10-031-403-1.rsp

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Search completed: March 24, 2003, 17:44:27
Job time : 12 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	384.5	52.7	149	4	Q96HK3 homo sapien
2	383.5	52.6	149	5	Q95NR9 metridium s
3	383.5	52.6	149	11	Q9D5G4 mus musculus
4	382.5	52.5	149	5	Q02367 clona intes
5	380.5	52.2	149	5	Q9UB37 brachiolesto
6	380.5	52.2	149	5	Q96081 halocynthia
7	379.5	52.1	149	5	Q9GRJ1 lumbricus r
8	379.5	52.1	149	5	Q16305 caenorhabdi
9	379.5	52.1	149	13	Q906D3 myxine giut
10	378.5	51.9	149	13	Q93410 gallus gall
11	377.5	51.8	149	5	Q97341 suberites d
12	375.5	51.5	146	5	Q94801 toxoplasma
13	375.5	51.5	156	5	Q8ST90 strongyloce
14	373.5	51.2	149	10	Q40302 macrocystis
15	373	51.2	152	4	Q13942 homo sapien
16	370.5	50.8	149	5	Q95N14 halichondri

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Db 121 EVDQMIREADIDGQGVNYEEFVQM 146

RESULT 2
Q95NR9
ID Q95NR9 PRELIMINARY; PRT; 149 AA.
AC Q95NR9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Calmodulin.
GN CAM.

OS Metridium senile (Brown sea anemone) (Fried sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Metridiidae; Metridium.
OX NCBI_TaxID=6116;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuasa H.J., Suzuki T., Yazawa M.;
RT "Structural organization of lower marine nonvertebrates calmodulin
RT genes";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDJB databases.
DR EMBL; AB063183; BAB61796.1; -.
DR EMBL; AB063181; BAB61794.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR SEQUENCE 149 AA; 16838 MW; 6B44A8917FD5927B CRC64;

Query Match 52.6%; Score 383.5; DB 5; Length 149;
Best Local Similarity 51.0%; Pred. No. 3.7e-24;
Matches 76; Conservative 32; Mismatches 38; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKFAFSAVDGNGTINAEALGALKATGKNLSEAQLKLISEVDSG 60
Db 1 MADQLTEQIAEFKFAFLFDKDGDTITTKELGTVMRSGLQNPTEAEALQDMINEVDAG 60

QY 61 DGEISFOEFLT-AARKAR--AGLEDLOVAFRAFDDGQGHITVDLRRAMAGLGQPLPOE 117
Db 61 NCTIDPPELTMMARKMDTSEEEIREAFRVFDKDGNGVISAELRHVMTNLGKLTDE 120

QY 118 ELDAMIREADVDDGRVNYEEFARM 146
Db 121 EVDQMIREADIDGQGVNYEEFVQM 149

RESULT 3
Q9D6G4
ID Q9D6G4 PRELIMINARY; PRT; 149 AA.
AC Q9D6G4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adult male hippocampus cDNA, RIKEN full-length enriched library,
DE clone:2900055023, full insert sequence.
GN CALM1 OR CALM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013695; BAB28959.1; -.
DR HSSP; P02593; 1AK8.
DR MGD; MGI:88251; Calm1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PD00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SEQUENCE 149 AA; 16851 MW; 6B4BC3FCD810679B CRC64;

Query Match 52.6%; Score 383.5; DB 11; Length 149;
Best Local Similarity 52.1%; Pred. No. 3.7e-24;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKFAFSAVDGNGTINAEALGALKATGKNLSEAQLKLISEVDSG 60
Db 1 MADQLTEQIAEFKFAFLFDKDGDTITTKELGTVMRSGLQNPTEAEALQDMINEVDAG 60

QY 61 DGEISFOEFLT-AARKAR--AGLEDLOVAFRAFDDGQGHITVDLRRAMAGLGQPLPOE 117
Db 61 NCTIDPPELTMMARKMDTSEEEIREAFRVFDKDGNGVISAELRHVMTNLGKLTDE 120

QY 118 ELDAMIREADVDDGRVNYEEFARM 143
Db 121 EVDQMIREADIDGQGVNYEEFLOM 146

RESULT 4
Q02367
ID Q02367 PRELIMINARY; PRT; 149 AA.
AC Q02367;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Calmodulin.
GN CAM.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7119;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98394335; PubMed=9727352;
RA Di Gregorio A., Villani M.G., Locascio A., Ristatore F., Aniello F.,
RA Branno M.;
RT "Developmental regulation and tissue-specific localization of
RT calmodulin mRNA in the protochordate Ciona intestinalis.";
RL Dev. Growth Differ. 40:387-394(1998).
DR EMBL; Y13578; CAA73906.1; -.
DR HSSP; P02593; 1AK8.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR SEQUENCE 149 AA; 16836 MW; 6B554EFDADF2E27B CRC64;

Query Match 52.5%; Score 382.5; DB 5; Length 149;
Best Local Similarity 51.7%; Pred. No. 4.4e-24;

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Matches 77; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDTCNGTINAEALGAALKATGKNLSEALRKLISEVDSG 60
DB 1 MADQLTEEQIAEFKAFSLFDKDGDTTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 60

QY 61 DGEISFOEFLT-AARKA--AGLEDQVAFRAFDDGDGHITVDLRRAMAGLGQPLPQE 117
DB 61 NGTIDPEFTLMARKMKDTSDEEIREAFRVFDKNGFISAAELRHVMTNLGKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARM146
DB 121 EVDEMIREADVDDGQVNYEEFVMTNK 149

RESULT 5
Q9UB37
ID Q9UB37 PRELIMINARY; PRT; 149 AA.
AC Q9UB37;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calmodulin 2.
GN CAM2.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20407449; PubMed=10948270;
RA Karabinos A., Bhattacharya D.;
RT "Molecular evolution of calmodulin and calmodulin-like genes in the
RT cephalochordate Branchiostoma.";
RL J. Mol. Evol. 51:141-148(2000).
DR EMBL; AJ133486; CAB38169.1; -.
DR HSSP; P02593; 1AK8.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFH; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 149 AA; 16824 MW; 3AABA8917FDD826D CRC64;

Query Match 52.2%; Score 380.5; DB 5; Length 149;
Best Local Similarity 50.3%; Pred. No. 6.5e-24;
Matches 75; Conservative 32; Mismatches 39; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDTCNGTINAEALGAALKATGKNLSEALRKLISEVDSG 60
DB 1 MADQLTEEQIAEFKAFSLFDKDGDTTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 60

QY 61 DGEISFOEFLT-AARKA--AGLEDQVAFRAFDDGDGHITVDLRRAMAGLGQPLPQE 117
DB 61 NGTIDPEFTLMARKMKDTSDEEIREAFRVFDKNGFISAAELRHVMTNLGKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARM146
DB 121 EVDEMIREADVDDGQVNYEEFVMTNK 149

RESULT 6
Q96081
ID Q96081 PRELIMINARY; PRT; 149 AA.
AC Q96081;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calmodulin B.
GN CAM B.
OS Halocynthia roretzi (Sea squirt).

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OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99196995; PubMed=10095116;
RA Yuasa H.J., Yamamoto H., Takagi T.;
RT "The structural organization of the ascidian, Halocynthia roretzi,
RT calmodulin genes. The vicissitude of introns during the evolution of
RT calmodulin genes.";
RL Gene 229:163-169(1999).
DR EMBL; AB018797; BAA33968.1; -.
DR HSSP; P02593; 1AK8.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFH; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 149 AA; 16841 MW; 9E5EED47FC703CA CRC64;

Query Match 52.2%; Score 380.5; DB 5; Length 149;
Best Local Similarity 52.1%; Pred. No. 6.5e-24;
Matches 76; Conservative 30; Mismatches 37; Indels 3; Gaps 2;

QY 1 MAGELTPEEAQYKAFSAVDTCNGTINAEALGAALKATGKNLSEALRKLISEVDSG 60
DB 1 MADQLTEEQIAEFKAFSLFDKDGDTTITTKELGTVMRSLGQNPTEAELQDMINEVDAG 60

QY 61 DGEISFOEFLT-AARKA--GLEDLQVAFRAFDDGDGHITVDLRRAMAGLGQPLPQE 117
DB 61 NGTIDPEFTLMARKMKDTSDEEIREAFRVFDKNGFISAAELRHVMTNLGKLTDE 120

QY 118 ELDMIREADVDDQGRVNYEEFARM143
DB 121 EVDEMIREADVDDGQVNYEEFVMTM 146

RESULT 7
Q9GRJ1
ID Q9GRJ1 PRELIMINARY; PRT; 149 AA.
AC Q9GRJ1;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calmodulin.
GN CALMODULIN.
OS Lumbricus rubellus (Humus earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=35632;
RN [1]
RP SEQUENCE FROM N.A.
RA Sturzenbaum S.R., Manova A., Morgan A.J., Kille P., Schaffner W.,
RA Georgiev O.;
RT "Earthworm cDNAs.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ291615; CAC14791.1; -.
DR HSSP; P02593; 1AK8.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFH; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 149 AA; 16841 MW; 6B44BFA17FC7027B CRC64;

Query Match 52.1%; Score 379.5; DB 5; Length 149;
Best Local Similarity 52.1%; Pred. No. 7.8e-24;
Matches 76; Conservative 30; Mismatches 37; Indels 3; Gaps 2;

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QY 1 MAGELTPEEAQYKKAFAVDTGNGTINAEGLGAALKATGKNLSEAQLKLISEVDSG 60
DB 1 MADQLTEEQIAEFAEFLDKDGGTITTKELGTVMRSLGQNPTEAEQLQDMINEVDAG 60
QY 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDDGCGHITVDELRAMAGLGQPLPOE 117
DB 61 NGTIDFPEFLTMMARKMDTDEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTD 120
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 121 EVDIMIREADIDGCGVNYEEFVTM 146

RESULT 8
O16305
ID O16305 PRELIMINARY; PRT; 149 AA.
AC O16305;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE T21H3.3 protein.
GN T21H3.3 OR CMD-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaiden N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Scheet P.;
RA Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Kraev A., Gazzotti P.;
RT "Expression and functional characterization of calmodulin from
RT Caenorhabditis elegans.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016429; AB65364.1; -.
DR EMBL; AJ332193; CAAL0601.1; -.
DR HSSP; P02593; IAK8.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 149 AA; 16924 MW; 6940B8917FC7027B CRC64;

Query Match 52.1%; Score 379.5; DB 5; Length 149;
Best Local Similarity 52.1%; Pred. No. 7.8e-24;
Matches 76; Conservative 30; Mismatches 37; Indels 3; Gaps 2;

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QY 1 MAGELTPEEAQYKKAFAVDTGNGTINAEGLGAALKATGKNLSEAQLKLISEVDSG 60
DB 1 MADQLTEEQIAEFAEFLDKDGGTITTKELGTVMRSLGQNPTEAEQLQDMINEVDAG 60
QY 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDDGCGHITVDELRAMAGLGQPLPOE 117
DB 61 NGTIDFPEFLTMMARKMDTDEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTD 120
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 121 EVDIMIREADIDGCGVNYEEFVTM 146

RESULT 9
Q9U6D3
ID Q9U6D3 PRELIMINARY; PRT; 149 AA.
AC Q9U6D3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Calmodulin.
GN CAM.
OS Myxine glutinosa (Atlantic hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Myxiniinae; Myxine.
OX NCBI_TaxID=7769;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA White G.P., Cunningham C.;
RT "Characterization of a cDNA encoding calmodulin from the Atlantic
RT hagfish (Myxine glutinosa).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187305; AAD56955.1; -.
DR HSSP; P02593; ICMG.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 149 AA; 16836 MW; 8BA5C31CD4BA78DB CRC64;

Query Match 52.1%; Score 379.5; DB 13; Length 149;
Best Local Similarity 51.4%; Pred. No. 7.8e-24;
Matches 75; Conservative 33; Mismatches 35; Indels 3; Gaps 2;

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QY 1 MAGELTPEEAQYKKAFAVDTGNGTINAEGLGAALKATGKNLSEAQLKLISEVDSG 60
DB 1 MADQLTEEQIAEFAEFLDKDGGTITTKELGTVMRSLGQNPTEAEQLQDMINEVDAG 60
QY 61 DGEISFOEFLT-AARKAR--AGLEDQVAFRAFDDGCGHITVDELRAMAGLGQPLPOE 117
DB 61 NGTIDFPEFLTMMARKMDTDEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTD 120
QY 118 ELDAMIREADVDDGRVNYEEFARM 143
DB 121 EVDIMIREADIDGCGVNYEEFVTM 146

RESULT 10
O93410
ID O93410 PRELIMINARY; PRT; 149 AA.
AC O93410;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Calmodulin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.
 RN NCBI_TaxID=9031;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=90281977; PubMed=2162134;
 RA Van Eldik L.J., Zimmer W.E., Barger S.W., Watterson D.M.;
 RT "perturbation of the calmodulin system in transformed cells.";
 RL Adv. Exp. Med. Biol. 269:111-120(1990).
 RP SEQUENCE FROM N.A.
 RA Van Eldik L.J., Zimmer W.E., Barger S.W., Watterson D.M.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF081672; RAC31608.1;
 DR HSSP: P02593; 1AK8.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 4.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; Eph; 4.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 SQ SEQUENCE 149 AA; 16852 MW; 6B4BC3FCD550C67B CRC64;
 Query Match 51.9%; Score 378.5; DB 13; Length 149;
 Best Local Similarity 50.7%; Pred. No. 9.5e-24;
 Matches 74; Conservative 34; Mismatches 35; Indels 3; Gaps 2;
 QY 1 MAGELTPEEAQYKAFSAVDGTGNGTINAQELGAALKATGKNLSEAQLKRLISEVDSG 60
 DB 1 MADQLTEEQIAEFAKFAFLDKDGDGTTTKELGTVMRSLGQNPTEAELQDMINEVDAG 60
 QY 61 DGEISFOEFLT-AARKAR--AGLEDIQVAFRFDQDGDGHITVDELRRAAGLQPLPQE 117
 DB 61 NGTIDPEFLTMARKMKDTSSEERAEAFVFDKDGNGYISAAELRHVMTNLGKLTDE 120
 QY 118 ELDAMIREADVDDGRVNYEEFARM 143
 DB 121 QVDEMIRESDIDGQGVNYEEFQVM 146
 RESULT 11
 ID O97341 PRELIMINARY; PRT; 149 AA.
 AC O97341;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Calmodulin.
 OS Suberites domuncula (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Hadromerida; Suberitidae; Suberites.
 OX NCBI_TaxID=55567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99191695; PubMed=10091595;
 RA Wimmer W., Petrovic S., Kruse M., Schroeder H.C., Krasko A., Batel R.,
 RA Mueller W.E.G.;
 RT "Evolutionary relationship of metazoa within the eukaryotes based on
 RT molecular data from porifera.";
 RL Proc. R. Soc. Lond. B, Biol. Sci. 0:0-0(0).
 RP SEQUENCE FROM N.A.
 RA Schuetz J., Reis Custodio M., Efreanova S.M., Mueller I.M.,
 RA Mueller W.E.G.;
 RT "Evolutionary relationship of metazoa within the eukaryotes based on
 RT molecular data from porifera.";
 RL Proc. R. Soc. Lond. B, Biol. Sci. 0:0-0(0).
 DR EMBL: Y18166; CAA77069.1;
 DR HSSP: P02593; 1AK8.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; Eph; 4.

DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 SQ SEQUENCE 149 AA; 16798 MW; 83EE891A0ACAB28F CRC64;
 Query Match 51.8%; Score 377.5; DB 5; Length 149;
 Best Local Similarity 51.0%; Pred. No. 1.1e-23;
 Matches 76; Conservative 30; Mismatches 40; Indels 3; Gaps 2;
 QY 1 MAGELTPEEAQYKAFSAVDGTGNGTINAQELGAALKATGKNLSEAQLKRLISEVDSG 60
 DB 1 MADQLTEEQIAEFAKFAFLDKDGDGTTTKELGTVMRSLGQNPTEAELQDMINEVDAG 60
 QY 61 DGEISFOEFLT-AARKAR--AGLEDIQVAFRFDQDGDGHITVDELRRAAGLQPLPQE 117
 DB 61 NGTIDPEFLTMARKMKDTSSEERAEAFVFDKDGNGFISAAELRHVMTNLGKLTDE 120
 QY 118 ELDAMIREADVDDGRVNYEEFARM 146
 DB 121 EVDEMIREADVDDGQGVNYEEFVGM 149
 RESULT 12
 ID O94801 PRELIMINARY; PRT; 146 AA.
 AC O94801;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Calmodulin (Fragment).
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RH;
 RX MEDLINE=99270320; PubMed=10340495;
 RA Seeber F., Beuerle B., Schmidt H.H.W.;
 RT "Cloning and functional expression of the Calmodulin gene from
 RT Toxoplasma gondii.";
 RL Mol. Biochem. Parasitol. 99:295-299(1999).
 DR EMBL: Y08373; CAA69660.1;
 DR HSSP: P02593; 1AK8.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PR00450; RECOVERIN.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; Eph; 4.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 FT NON_TER 146
 SQ SEQUENCE 146 AA; 16474 MW; E7D37EC3A9ACE7AF CRC64;
 Query Match 51.5%; Score 375.5; DB 5; Length 146;
 Best Local Similarity 52.1%; Pred. No. 1.6e-23;
 Matches 76; Conservative 30; Mismatches 37; Indels 3; Gaps 2;
 QY 1 MAGELTPEEAQYKAFSAVDGTGNGTINAQELGAALKATGKNLSEAQLKRLISEVDSG 60
 DB 1 MADQLTEEQIAEFAKFAFLDKDGDGTTTKELGTVMRSLGQNPTEAELQDMINEVDAG 60
 QY 61 DGEISFOEFLT-AARKAR--AGLEDIQVAFRFDQDGDGHITVDELRRAAGLQPLPQE 117
 DB 61 NGTIDPEFLTMARKMKDTSSEERAEAFVFDKDGNGFISAAELRHVMTNLGKLTDE 120
 QY 118 ELDAMIREADVDDGRVNYEEFARM 143
 DB 121 EVDEMIREADVDDGQGVNYEEFVGM 146
 RESULT 13
 ID Q8STF0 PRELIMINARY; PRT; 156 AA.
 AC Q8STF0;

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1  MAGELTPEEEAAQYKKAFSAVDTDCNGTINAQELGAALKATCKNLSAQRLKLISEVDSG 60
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1  MADOLTEEOIAEFKEAFSLFDKPDGDTITTKELGTWMSLGONPTEAFLODMTNEVDAGS 60

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115 PQEELDAMIREADVDQDGRVNYEEFARM 143
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121

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